

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 28, 2004, 12:59:15 ; Search time 579 Seconds

(without alignments)

2702.629 Million cell updates/sec

Title: US-10-017-084A-523

Perfect score: 2408

Sequence: 1 MKTIQPKMHSISWAIPTGL.....RRAGCVWLLPLVLHLLKF 344

Scoring table:

BLOSUM30
Xgapop 1.0 , Xgapext 0.1
Ygapop 1.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2960401 seqs, 2274450654 residues

Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

-MODEL=framer_p2n.model -DB=xlh
-Q=/cgn2_1/USPTO.spool/US10017084/runat_28052004_125908_29931/app_query.fasta_1.519
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum30
-TRANS=human40.cdi -LIST=100 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10017084 @CGN 1.1 481 @runat_28052004_125908_29931
-NCPU=6 -ICPU=3 -NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEU TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=1 -XGAPEXT=0.1
-Fgapop=6 -Fgapext=7 -Ygapop=1 -Ygapext=0.1 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:
10: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:
11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:
14: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:
15: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:
16: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:
17: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:
18: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:
19: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
---------------	-------	----------------	--------	----	-------------

1	2408	100.0	1032	13	US-10-657-103-1	Sequence 1, Appl1
2	2408	100.0	1679	9	US-09-978-295A-522	Sequence 522, App
3	2408	100.0	1679	9	US-09-978-637-522	Sequence 522, App
4	2408	100.0	1679	9	US-09-978-192A-522	Sequence 522, App
5	2408	100.0	1679	9	US-09-999-832A-522	Sequence 522, App
6	2408	100.0	1679	10	US-09-978-189-522	Sequence 522, App
7	2408	100.0	1679	10	US-09-978-608A-522	Sequence 522, App
8	2408	100.0	1679	10	US-09-978-585A-522	Sequence 522, App
9	2408	100.0	1679	10	US-09-978-191A-522	Sequence 522, App
10	2408	100.0	1679	10	US-09-978-403A-522	Sequence 522, App
11	2408	100.0	1679	10	US-09-999-833A-522	Sequence 522, App
12	2408	100.0	1679	10	US-09-981-915A-522	Sequence 522, App
13	2408	100.0	1679	10	US-09-978-824-522	Sequence 522, App
14	2408	100.0	1679	10	US-09-318-585A-522	Sequence 522, App
15	2408	100.0	1679	10	US-09-978-423A-522	Sequence 522, App
16	2408	100.0	1679	10	US-09-978-193A-522	Sequence 522, App
17	2408	100.0	1679	10	US-09-999-830A-522	Sequence 522, App
18	2408	100.0	1679	10	US-09-978-757A-522	Sequence 522, App
19	2408	100.0	1679	10	US-09-978-187B-522	Sequence 522, App
20	2408	100.0	1679	10	US-09-978-643A-522	Sequence 522, App
21	2408	100.0	1679	10	US-09-978-375A-522	Sequence 522, App
22	2408	100.0	1679	10	US-09-978-298A-522	Sequence 522, App
23	2408	100.0	1679	10	US-09-978-188A-522	Sequence 522, App
24	2408	100.0	1679	10	US-09-978-681A-522	Sequence 522, App
25	2408	100.0	1679	10	US-09-978-194A-522	Sequence 522, App
26	2408	100.0	1679	10	US-09-999-829A-522	Sequence 522, App
27	2408	100.0	1679	10	US-09-978-299A-522	Sequence 522, App
28	2408	100.0	1679	10	US-09-978-544A-522	Sequence 522, App
29	2408	100.0	1679	10	US-09-978-665A-522	Sequence 522, App
30	2408	100.0	1679	10	US-09-978-802A-522	Sequence 375, App
31	2408	100.0	1679	13	US-10-147-493-375	Sequence 375, App
32	2408	100.0	1679	13	US-10-164-749A-522	Sequence 522, App
33	2408	100.0	1679	13	US-10-145-127-375	Sequence 375, App
34	2408	100.0	1679	13	US-10-160-503-375	Sequence 375, App
35	2408	100.0	1679	13	US-10-143-118-375	Sequence 375, App
36	2408	100.0	1679	13	US-10-144-993-375	Sequence 375, App
37	2408	100.0	1679	13	US-10-158-787-375	Sequence 375, App
38	2408	100.0	1679	13	US-10-081-056-55	Sequence 125, App
39	2408	100.0	1679	13	US-10-219-535-125	Sequence 125, App
40	2408	100.0	1679	13	US-10-232-230-125	Sequence 125, App
41	2408	100.0	1679	13	US-09-999-831A-522	Sequence 522, App
42	2408	100.0	1679	13	US-10-140-024-375	Sequence 375, App
43	2408	100.0	1679	13	US-10-013-917A-522	Sequence 375, App
44	2408	100.0	1679	13	US-10-140-808-375	Sequence 522, App
45	2408	100.0	1679	13	US-09-999-834A-522	Sequence 522, App
46	2408	100.0	1679	13	US-10-232-224-125	Sequence 125, App
47	2408	100.0	1679	13	US-10-152-405-375	Sequence 375, App
48	2408	100.0	1679	13	US-10-162-521A-522	Sequence 522, App
49	2408	100.0	1679	13	US-10-127-852A-375	Sequence 375, App
50	2408	100.0	1679	13	US-10-127-900A-375	Sequence 375, App
51	2408	100.0	1679	13	US-10-128-685A-375	Sequence 375, App
52	2408	100.0	1679	13	US-10-131-820A-375	Sequence 375, App
53	2408	100.0	1679	13	US-10-142-886-375	Sequence 375, App
54	2408	100.0	1679	13	US-10-145-016A-522	Sequence 522, App
55	2408	100.0	1679	13	US-10-145-088A-522	Sequence 522, App
56	2408	100.0	1679	13	US-10-145-092A-522	Sequence 522, App
57	2408	100.0	1679	13	US-10-145-129A-522	Sequence 522, App
58	2408	100.0	1679	13	US-10-146-728-375	Sequence 375, App
59	2408	100.0	1679	13	US-10-146-786-375	Sequence 375, App
60	2408	100.0	1679	13	US-10-147-499-375	Sequence 375, App
61	2408	100.0	1679	13	US-10-157-798-375	Sequence 375, App
62	2408	100.0	1679	13	US-10-165-038A-522	Sequence 522, App
63	2408	100.0	1679	13	US-10-165-353A-522	Sequence 522, App
64	2408	100.0	1679	13	US-10-167-600-522	Sequence 522, App
65	2408	100.0	1679	13	US-10-170-481A-522	Sequence 522, App
66	2408	100.0	1679	13	US-10-172-039A-522	Sequence 522, App
67	2408	100.0	1679	13	US-10-210-028-522	Sequence 55, Appl1
68	2408	100.0	1679	13	US-10-305-654-55	Sequence 55, Appl1
69	2408	100.0	1679	14	US-10-066-500-103	Sequence 103, App
70	2408	100.0	1679	15	US-10-028-072-375	Sequence 375, App
71	2408	100.0	1679	15	US-10-121-049-375	Sequence 375, App
72	2408	100.0	1679	15		

73 2408 100.0 1679 15 US-10-123-904-375 Sequence 375, App
74 2408 100.0 1679 15 US-10-140-470-375 Sequence 375, App
75 2408 100.0 1679 15 US-10-175-746-375 Sequence 375, App
76 2408 100.0 1679 15 US-10-176-918-375 Sequence 375, App
77 2408 100.0 1679 15 US-10-176-918-375 Sequence 375, App
78 2408 100.0 1679 15 US-10-227-884-125 Sequence 125, App
79 2408 100.0 1679 15 US-10-002-796-103 Sequence 103, App
80 2408 100.0 1679 15 US-10-066-273-103 Sequence 103, App
81 2408 100.0 1679 15 US-10-066-494-103 Sequence 103, App
82 2408 100.0 1679 15 US-10-137-865-375 Sequence 375, App
83 2408 100.0 1679 15 US-10-140-474-375 Sequence 375, App
84 2408 100.0 1679 15 US-10-142-431-375 Sequence 375, App
85 2408 100.0 1679 15 US-10-143-114-375 Sequence 375, App
86 2408 100.0 1679 15 US-10-230-163-125 Sequence 125, App
87 2408 100.0 1679 15 US-10-140-002-375 Sequence 375, App
88 2408 100.0 1679 15 US-10-066-269-103 Sequence 103, App
89 2408 100.0 1679 15 US-10-066-211-103 Sequence 103, App
90 2408 100.0 1679 15 US-10-066-193-103 Sequence 103, App
91 2408 100.0 1679 15 US-10-230-338-125 Sequence 125, App
92 2408 100.0 1679 15 US-10-142-419-375 Sequence 375, App
93 2408 100.0 1679 15 US-10-218-631-125 Sequence 125, App
94 2408 100.0 1679 15 US-10-017-081A-522 Sequence 522, App
95 2408 100.0 1679 15 US-10-123-262-375 Sequence 375, App
96 2408 100.0 1679 15 US-10-142-423-375 Sequence 375, App
97 2408 100.0 1679 15 US-10-230-414-125 Sequence 125, App
98 2408 100.0 1679 15 US-10-121-050-375 Sequence 375, App
99 2408 100.0 1679 15 US-10-141-755-375 Sequence 375, App
100 2408 100.0 1679 15 US-10-167-749-522 Sequence 522, App

ALIGNMENTS

RESULT 1
US-10-657-103-1
; Sequence 1, Application US/10657103
; Publication No. US20040038285A1
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. US20040038285A1el Polypeptides, cDNA encoding the same, and u
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/10/657,103
; CURRENT FILING DATE: 2003-09-09
; PRIOR FILING DATE: US/09/700,397
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-657-103-1

Alignment Scores:
Pred. No.: 9,93e-43 Length: 1032
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-017-084A-523 (1-344) x US-10-657-103-1 (1-1032)

Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
Db 1 ATGAAACCAATCCAGCCAAAATGACAAATCTCTTGGCAATCTTCAGCGGGCTG 60
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 61 GCTGCTGTGTCTCTTCCAGAGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCCAAA 120

Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 121 GCTATGGCAACAGTACCGTCCGGCAGGGAGAGCGCCACCTCAGGTGCACATTTGAC 180
Qy 61 AsnArgValThrArgValAlaIleTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
Db 181 AACCGGCTCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATCTGGGAATGAC 240
Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
Db 241 AAGTGTGCTCGATCTCGCTGGTCTCTTCTGAGCAACACCAACGAGTACAGCATC 300
Qy 101 GlnIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 301 GAGATCCAGACGATGATGTATGACGAGGGCCCTTACCTGCTCGGTGCGAGACAGAC 360
Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 361 AACCCACCAAGACCTCTAGGGTCCACCTCAATGTGCAAGTATCTCCCAAAATTTGAGAG 420
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 421 ATTCTCTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCACT 480
Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 481 GGTAGACACAGGCTACGGTTACTTGGAGACACATCTCTCCCAAGGGTGGCTTTGTG 540
Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGlnSerGlyAspTyrGlu 200
Db 541 AGTGAAGACGAATACCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGACTACGAG 600
Qy 201 CysSerAlaSerAsnAspValAlaIleProValValArgArgValLysValThrValAsn 220
Db 601 TGCAGTGCCTCCAAATGACGTGGCGCGCGGTGGTACGGAGAGTAAGGTACCGTGAAC 660
Qy 221 TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 661 TATCCACCATACATTTCCAGAGCAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 720
Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
Db 721 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAA 780
Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 781 AGACTGATTGAGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTCTCTCAAACTC 840
Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db 841 ATCTTCTCAATGTCTCTGAACATGACTATGGGAACCTACACTTGCCTGGGCTCCCAACAG 900
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 901 CTGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGTCAGGAGGTGAGC 960
Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
Db 961 AACGGCAGCTGAGGAGGGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Qy 341 LeuLeuLysPhe 344
Db 1021 CTCTCAAAATTT 1032

RESULT 2

US-09-978-295A-522
; Sequence 522, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558

```

; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 1,19e-41 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-295A-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB 134 ATGAARACCATCCAGCCAAATATCAATTCATCTCTGGGCAATCTTCACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTGTGTCTCTTCACAGGAGTCCCGTGGCAGCGGAGATGCCACCTTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCACCTTCAGGTGACATTATGAC 313
QY 61 AsnArgValThrArgValAlaThrIleAsnArgSerThrIleLeuValAlaGlyAsnAsp 80
DB 1154 CTTCTCAAAATTT 1165

RESULT 3
US-09-978-697-522
; Sequence 522, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT:

314 AACCGGGTCACCCGGGTGGCCTGCTGCTAAACCCAGACACCATCTCTATGCTGGGAATGAC 373
81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlySerIle 100
374 AAGTGTGCTCGATCCCTCGGTGGTCTCTTGAGCAACACCCAAACCGAGTACAGATC 433
101 GluIleGlnAsnValAspValIleAspGluGlyProTyrThrCysSerValGlnThrAsp 120
434 GAGATCCAGAACGCTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGTGACAGAC 493
121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
494 AACCAACCAAGACCTTAGGGTCCACCTCAATGTGTGAAGTATCTCCCAAAATTTAGAG 553
141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
554 ATTCTTTCAGATATCTCCATTAATGAGGAAACAATATTAGCTTCACTGCATAGCAACT 613
161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
614 GGTAGACCCAGAGCCTACGGTTACTTTGGAGACACATCTCTCCCAAGCGTGGCTTTGTG 673
181 SerGluAspGluTyrIleGluIleGlnGlyIleThrArgGluGlnSerGlyAspThrGlu 200
674 AGTGAAGACGATATCTGGAATTCAGGGCATCACCCCGGAGCAGTCAGGGGACTACGAG 733
201 CysSerAlaSerAsnAspValAlaProValValArgValIleValIleValValAsn 220
734 TGCAGTGCCTCCATGACGTGGCCCGGCCCTGGTACGGAGAGTAAGGTACCGTGAC 793
221 TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnIleLysGlyThr 240
794 TATCCACCATACATTTTCAGAGCCCAAGGTACAGGTGTCCCGGTGGGACAAAGGGGACA 853
241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIleAspAspLys 260
854 CTGCAGTGTGAAGCCTTCAGCAGTCCCTCCAGCAGAAATTCAGGTGGTACAGGATGACAA 913
261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
914 ACACCTGATTGAAGGAAAGAGGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 973
281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
974 ATCTTCTTCAATGTCTCTCAACATGACTATGGAACTACACTTGGGTGGCTCCACAAAG 1033
301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyValValSerGluValSer 320
1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGGCCCGTCCAGGAGGTGAGC 1093
321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
1094 AACGGCACGTGAGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1153
341 LeuLeuLysPhe 344
DB 1154 CTTCTCAAAATTT 1165
```


APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30

PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 1, 19e-41
Score: 2408.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 9

US-10-017-084a-523 (1-344) x US-09-978-697-522 (1-1679)

Qy 1 MetLysThrLeGlnProLysMetHisAsnSerLeSerTrpAlaIlePheThrGlyLeu 20
Db 134 ATGAAACCATCCAGCCAAAATGACAAATTCATCTCTGGGCAATCTTCACCGGGGCTG 193
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTGTCTCTCCAGAGAGTCCCGTGGCAGCGAGATGCCACCTTCCCAA 253
Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGGACAACGTACCGTCCGGCAGGGGAGAGCGCACCTCAGGTGCACTATTGAC 313
Qy 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp 80
Db 314 AACCGGGTCACCGGGTGGCTGGTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTySerIle 100
Db 374 AAGTGGTGGCTGGATCTCTCGCGTGGTCTCTTGAGCAACACCAACGAGTACGATC 433
Qy 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyThrCysSerValGlnThrAsp 120

Db 434 GAGATCCAGAACGTGGATGTGTATGACGAGGCGCCTTACACCTGCTCGGTGCAGACAGAC 493
Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCAACCAAGACCTCTAGGTCCTCAGCTTGTGCAAGTATCTCCCAAAATTTAGAG 553
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTTCTTCAGATATCTCCATTATGAGGGAACAATATTAGCTCACCTGCATGCACTACT 613
Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACCAAGACCTTACGTTACTTTGGAGACACATCTCTCCCAAGCGGTTGGTGTG 673
Qy 181 SerGluAspGluTyIleuGluIleGlnGlyThrArgGluGlnSerGlyAspTyIleGlu 200
Db 674 AGTGAAGACGAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAAGGAGTACGAG 733
Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
Db 734 TGCAGTGCCTCCATGACGTGCGCGCCCGTGGTACGAGAGTAAAGGTCAACCTGAAC 793
Qy 221 TyrProTyroTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCCACCACATATTCAGAGCAAGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyIleTyIleAspAspLys 260
Db 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATCCAGTGGTACAGGATGACAAA 913
Qy 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTTGAAGAAAGAAAGGGGTGAAGTGAAGAAACAGACCTTCTCTCAAAATC 973
Qy 281 IlePhePheAsnValSerGluHisAspTyIleGlyAsnTyThrCysValAlaSerAsnLys 300
Db 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACATACACTTGGCGGCTCCAAACAG 1033
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1034 CTGGGCCACACCAATGCCAGCATCACTATTGGTCCAGGCCCTCAGCGAGGTGAGC 1093
Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
Db 1094 AACGGCAGGTCCAGGAGGAGGAGGCTGCGTCTGGCTGCTGCTCTTCTGGTCTTGACCTG 1153
Qy 341 LeuLeuLysPhe 344
Db 1154 CTTCTCAAAATTT 1165

RESULT 4

US-09-978-192A-522
; Sequence 522, Application US/09978192A
; Patent No. US2002017553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.

APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637

; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084639
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084640
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084598
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084600
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084627
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084643
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/085339
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085338
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085323
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085582
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085700
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085689
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
 Pred. No.: 1,19e-41 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-017-084a-523 (1-344) x US-09-978-192A-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTyrAlaIlePheThrGlyLeu 20
 DB 134 ATGAAACCATCCAGCCAAATGCAATTTCTATCTTGGCAATCTTCAGGGGCTG 193
 QY 21 AlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTCTGTCTCTTCCAAAGAGTGCCCGTCGCGAGGGAGATGCCACCTTCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 DB 254 GCTATGGAACAACGTGACGGTCCGGCAGGAGGAGCGCCACCCCTCAGGTGCACTATTGAC 313
 QY 61 AsnArgValThrArgValAlaTyrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
 DB 314 AACCGGGTCACCGGGTGGCTGGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
 QY 81 LysTyrCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 DB 374 AAGTGGTCTGTGATCTCTCGGTGGTCTTCTGAGCAACACCCCAACCGCAGTACAGCATC 433
 QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 DB 434 GAGATCAGAACCGTGGATGTTATGACGAGGGGCCCCCTTACACCTGCTCGGTGCGACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACCAACCAAGACCTTACGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553

QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTTCTTCAGATAICTCCATTAATGAAGGAACAATATTAGCTCCTCCTGCTAGCAACT 613
 QY 161 GlyArgProGluProThrValThrTyrArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACCAGAGCCTTACGGTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 673
 QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 DB 674 AGTGAAGACGAATATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAAGGGGATAC 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValValValValValValAsn 220
 DB 734 TGCAGTGGCTCCATGACGTGGCGCGCCCGTGGTACGAGAGTAAAGGTCAACGTGAAC 793
 QY 221 TyrProTyrIleSerGluAlaIleGlyThrGlyValProValGlyGlnIleGlyThr 240
 DB 794 TATCCACCATACATTTCCAGAAAGCCAAAGGTACAGGTGTCCCGCTGGGACAAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAspAspLys 260
 DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGATTCCTCAGAGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 DB 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAAACAGACCTTTCTCTCAAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 DB 974 ATCTTCTTCAATGTCTCTGAAACATGACTATGGGAACACTTGCCTGGCGCTCCAAACAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGGCCACACCATGCCAGCATCATGCTATTTGGTCAGGGCCCTGACGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgAlaGlyCysValTyrLeuLeuProLeuLeuValLeuHisLeu 340
 DB 1094 AACGGCACGTGAGGAGGGGAGGCTGCTGCTGGCTGCTGCTTCTTGTCTTGCACCTG 1153
 QY 341 LeuLeuLysPhe 344
 DB 1154 CTTCTCAAAATTT 1165

RESULT 5
 US-09-999-832A-522
 ; Sequence 522, Application US/09999832A
 ; Publication No. US20020192706A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07

; PRIOR APPLICATION NUMBER: 60/084600
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084627
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084643
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/085339
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085338
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085323
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085582
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085700
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085689
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 1,19e-41 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-017-084a-523 (1-344) x US-09-999-832A-522 (1-1679)

Qy 1 MetIysThrLeGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 Db 134 ATGAAACCACTCCAGCCAAATATCTATCTCTTGGGCAATCTTTCAGGGGCTG 193
 Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 Db 194 GCTGCTGTGTCTCTTCCAGGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCCAAA 253
 Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 Db 254 GCTATGACACACGTGACGGTCCGCGAGGGGAGAGCGCCCTCAGGTGCACATTTGAC 313
 Qy 61 AsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
 Db 314 AACCGGTTCACCCGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
 Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 Db 374 AAGTGGTGCCTGGATCTCTGGGTCTCTGAGCAACACCCAAACGCGATGACGATC 433
 Qy 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 Db 434 GAGATCCAGACGCGTGGATGTGTATGACGAGGGCCCTTACACTCTGCTGGTGCACAGAC 493
 Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 Db 494 AACCAACCAAGACCTCTAGGCTCCACCTATTGTGCAAGTATCTCCCAAAATTTAGAG 553
 Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 Db 554 ATTTCCTCAGATATCTCCATTAAAGAGGGAACCAATATTAGCCCTACCTGATAGCACT 613
 Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 Db 614 GGTAGACACGAGCCTACCGTTACTTGTGGAGACACATCTCTCCCAAGCGGTGGCTTGTG 673

Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 Db 674 AGTGAAGCAGATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCACGGGACTACGAG 733
 Qy 201 CysSerAlaSerAsnAspValAlaProValValArgArgValValValThrValAsn 220
 Db 734 TGCAGTGGCTCCCAATGACGTGGCCGCGCTGGTGTACGGAGAGTAAAGGTCCCGTGAAC 793
 Qy 221 TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 Db 794 TATCACCACATATTCAGAACCAAGGTGTCAGGTGTCCCGTGGGACAAAGGGGACA 853
 Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIleLysAspAspLys 260
 Db 854 CTGCACTGTGAGGCTTCAGCAGTCCCTCAGCAGAAATTCAGTGGGTACAGGATGACAAA 913
 Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheIleuSerLysLeu 280
 Db 914 AGACTGATTTGAAGGAAAGAAAGGGGTGAAGTGGAAACAGACCTTCTCTCAAAACTC 973
 Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 Db 974 ATCTTCTTCAATGCTCTCTGACATGACTATGGAACTACACTTGCCTGGCTCCACAG 1033
 Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 Db 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGGCGCTCAGCGAGGTGAGC 1093
 Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
 Db 1094 ACGGCACGTCCAGGAGGGGAGGAGCTCGTCTGGCTGCTGCTCTTCTGTGTTCACCTG 1153
 Qy 341 LeuLeuLysPhe 344
 Db 1154 CTCTCAAAATTT 1165

RESULT 6

US-09-978-189-522
 ; Sequence 522, Application US/09978189
 ; Publication No. US20030004102A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630P1C7
 ; CURRENT APPLICATION NUMBER: US/09/978,189

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89</											


```
; PRIOR FILLING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILLING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILLING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILLING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILLING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILLING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILLING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILLING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILLING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILLING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 1.19e-41 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-017-084a-523 (1-344) x US-09-978-189-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
Db 134 ATGAAACCACTCCAGCAAAATGCAATCTCTCTGGCAATCTTCACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTCTCTCTCAAGAGAGTGCCTGCGGAGGAGGAGCGCCACCTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGGACAACGTGACGGTCCGGAGGGAGGAGCGCCACCTCAGGTGCATATGTAC 313
QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTrpAlaGlyAsnAsp 80
Db 314 AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIle 100
Db 374 AGTGTGCTGTGATCCTCGCGTGGTCTCTGAGCAACACCCAAACGCGAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTrpAspGluGlyProTrpThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAACGTGGATGTGTATGACAGGGGCCCTTACCTGCTCGGTGAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCCCAAGACCTTAGGTGCCACCTCATTTGTCAAGTATCTCCCAAAATTTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTCTTCAGATATCTCATTAATGAAGGAAACAATATTAGCTCCTACCTGCATAGCAACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACCAAGCTACGGTTACTTGGAGACACATCTCTCCAAAGGGGTTCGCTTTG 673
QY 181 SerGluAspGlnTrpLeuGluIleGlnGlyIleThrArgGlnSerGlyAspTrpGlu 200
Db 674 AGTGAAGACCAATACTTGGAAATTCAGGGCATCCCGGAGCAGTCAGGGGACTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValValValValValVal 220
```

```
Db 734 TGCAGTGCCTCCATGACGTGGCGCGCGGTGTTACGAGAGTAAGGTCAACCGTGAAC 793
QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCCACCACATATTTCAAGAGCCCAAGGTA CAGGTGTCCCGCGTGGGACAAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIleAspAspLys 260
Db 854 CTGCGAGTGTGAAGCCTTCAGCAGTCCCTCAGCAGCAATCCAGTGTGTACAGGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGTGAAGAAACAGACCTTTCTCTCAAAACTC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTrpThrCysValAlaSerAsnLys 300
Db 974 ATCTTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGCTGCCCTCCCAACAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyValAlaValSerGluValSer 320
Db 1034 CTGGGCCACACCAATGCCAGCATCATGTATTTGGTCCAGGGCCCGTCCAGCGAGGTGACC 1093
QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
Db 1094 AACGGCACGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1153
QY 341 LeuLeuLysPhe 344
Db 1154 CTTCTCAAAATTT 1165

RESULT 7
US-09-978-608A-522
; Sequence 522, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
```

US-09-978-608A-522

Alignment Scores:

Pred. No.: 1.19e-41 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-608A-522 (1-1679)

Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
Db 134 ATGAACCAATCCAGCAGCAAAATGCAATCTCTTGGCAATCTTCAOGGGGTG 193
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTGTCTCTTCCAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAA 253
Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGGACAACGTGACGCTCGGCGGGGAGAGCCACCTCAGGTGCACATTATGAC 313
Qy 61 AsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp 80
Db 314 AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrSerIle 100
Db 374 AAGTGGTCCCTGGATCCCTCGGTGTCTCTTCTAGCAACACCCAAACGAGTACAGCATC 433
Qy 101 GluIleGlnAsnValAspValTyArgGluGlyProTyThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGACGTGGATGTATGACGAGGSCCTTACCTGCTCGGTGAGACACAC 493
Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCAACCAAGACCTTAGGTCCACCTCTTGTGCAAGTATCTCCCAAAATGTAGAG 553
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTTCTTCAGATATCTCATTAATGAAGGGAACAATATTAGCTCACCCTGCATAGCACT 613
Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACCAAGACCTACGGTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
Qy 181 SerGluAspGluTyLeuGluIleGlnGlyLeThrArgGluGlnSerGlyAspTyGlu 200
Db 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCGGAGCAGTCAGGGGACTACGAG 733
Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValIysValThrValAsn 220
Db 734 TGCAGTGCTCCATAGAGTGGCCGCGCGGTACGGAGAGTAAGGTACCGGTGAAC 793
Qy 221 TyrProTrpTyIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCCACCATATATTCAGAGCCAGAGGTACAGGTGTCCCGGTGGGCAAAAGGGGACA 853
Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyLeuAspAspLys 260
Db 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAATTCAGTGGTACAAAGATGACAAA 913
Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerIysLeu 280
Db 914 AGACTGATGTGAAGAAAGAAAGGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 973
Qy 281 IlePhePheAsnValSerGluHisAspTyIleGlyAsnTyThrCysValAlaSerAsnLys 300
Db 974 ATCTCTTCAATGTCTCTGAACATGACTATGGGAACACTACCTTGGCTGGCTCCCAAG 1033
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320

Db 1034 CTGGGCACACCAATGCAGCATCATGTATTGGTCAGGCGGTGAGGAGGTGAGC 1093
Qy 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
Db 1094 AACGGCAGCTGAGGAGGAGGAGGCTGGCTCTGGCTGTGCTCTTCTGTCTTGCACCTG 1153
Qy 341 LeuLeuLysPhe 344
Db 1154 CTTCTCAAAATTT 1165

RESULT 8

US-09-978-585A-522
; Sequence 522, Application US/09978585A
; Publication No. US20030049633A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; PRIORITY FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-978-585A-522

Alignment Scores:

Pred. No.: 1.19e-41 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-585A-522 (1-1679)

Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
Db 134 ATGAACCAATCCAGCAGCAAAATGCAATCTCTTGGCAATCTTCAOGGGGTG 193
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTGTCTCTTCCAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAA 253

QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGGACACGTGACGGTCCGGCAGGGGAGAGCCACCTTCAGTGCATATTGAC 313
QY 61 AsnArgValThrArgValAlaIleValLeuAsnArgSerThrIleLeuValAlaGlyAsnAsp 80
Db 314 AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCAGCACCCTCTCTATGCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnThrSerIle 100
Db 374 AAGTGGTGGCTGGATCCTCGGTGGTCTCTGAGCAACACCCAAACGGCAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGTGGCAGACGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTGTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCCTGCATAGCAACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACCAAGCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
QY 181 SerGluAspGlnTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
Db 674 AGTGAAGACCAATACTTGGAAATTCAGGGCATCACCGGGAGCAGTCAAGGGGACACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValValValValValVal 220
Db 734 TGCAAGTCCCTCCATGACGTGGCGCGCGCGGTGTACGAGAGTAAAGGTACCGTGAAC 793
QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCCACCATACATTTTCAAGAACCCAGGGTACAGGTGTCTCCCGTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
Db 854 CTGCAAGTGTGAAGCCTCAGCAGTCCCTCCAGCAATTCAGATGGTCAAGAGTACAA 913
QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTGAAGAAAGAGGGGTGAAGTGAAGAACAGACCTTCTCTCAAACTC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db 974 ATCTCTCTCAATGTCTCTGAACATGACTATGGGAACCTACACTTGGCGTGGCTCCAA 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1034 CTGGGCCACCAATGCGCATCATCTATTGGTCCAGCGCGCGTCAAGGAGGTGAGC 1093
QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340
Db 1094 AACGGCAGTCCAGAGGGGAGGCTGGCTGTGGCTGTCTCTCTCTCTCTCTCTCTCT 1153
QY 341 LeuLeuLysPhe 344
Db 1154 CTCTCAAAATTT 1165

RESULT 9

US-09-978-191A-522

; Sequence 522, Application US/09978191A

; Publication No. US20030050239A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27

/ PRIOR APPLICATION NUMBER: 60/079920
/ PRIOR FILING DATE: 1998-03-30
/ PRIOR APPLICATION NUMBER: 60/079923
/ PRIOR FILING DATE: 1998-03-30
/ PRIOR APPLICATION NUMBER: 60/080105
/ PRIOR FILING DATE: 1998-03-31
/ PRIOR APPLICATION NUMBER: 60/080107
/ PRIOR FILING DATE: 1998-03-31
/ PRIOR APPLICATION NUMBER: 60/080165
/ PRIOR FILING DATE: 1998-03-31
/ PRIOR APPLICATION NUMBER: 60/080194
/ PRIOR FILING DATE: 1998-03-31
/ PRIOR APPLICATION NUMBER: 60/080327
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/080328
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/080333
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/080334
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/081070
/ PRIOR FILING DATE: 1998-04-08
/ PRIOR APPLICATION NUMBER: 60/081049
/ PRIOR FILING DATE: 1998-04-08
/ PRIOR APPLICATION NUMBER: 60/081071
/ PRIOR FILING DATE: 1998-04-08
/ PRIOR APPLICATION NUMBER: 60/081195
/ PRIOR FILING DATE: 1998-04-08
/ PRIOR APPLICATION NUMBER: 60/081203
/ PRIOR FILING DATE: 1998-04-09
/ PRIOR APPLICATION NUMBER: 60/081229
/ PRIOR FILING DATE: 1998-04-09
/ PRIOR APPLICATION NUMBER: 60/081955
/ PRIOR FILING DATE: 1998-04-15
/ PRIOR APPLICATION NUMBER: 60/081817
/ PRIOR FILING DATE: 1998-04-15
/ PRIOR APPLICATION NUMBER: 60/081819
/ PRIOR FILING DATE: 1998-04-15
/ PRIOR APPLICATION NUMBER: 60/081952
/ PRIOR FILING DATE: 1998-04-15
/ PRIOR APPLICATION NUMBER: 60/081838
/ PRIOR FILING DATE: 1998-04-15
/ PRIOR APPLICATION NUMBER: 60/082568
/ PRIOR FILING DATE: 1998-04-21
/ PRIOR APPLICATION NUMBER: 60/082569
/ PRIOR FILING DATE: 1998-04-21
/ PRIOR APPLICATION NUMBER: 60/082704
/ PRIOR FILING DATE: 1998-04-22
/ PRIOR APPLICATION NUMBER: 60/082804
/ PRIOR FILING DATE: 1998-04-22
/ PRIOR APPLICATION NUMBER: 60/082700
/ PRIOR FILING DATE: 1998-04-22
/ PRIOR APPLICATION NUMBER: 60/082797
/ PRIOR FILING DATE: 1998-04-22
/ PRIOR APPLICATION NUMBER: 60/082796
/ PRIOR FILING DATE: 1998-04-23
/ PRIOR APPLICATION NUMBER: 60/083336
/ PRIOR FILING DATE: 1998-04-27
/ PRIOR APPLICATION NUMBER: 60/083322
/ PRIOR FILING DATE: 1998-04-28
/ PRIOR APPLICATION NUMBER: 60/083392
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083495
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083496
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083499
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083545
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083554
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083558

/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083559
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083500
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083742
/ PRIOR FILING DATE: 1998-04-30
/ PRIOR APPLICATION NUMBER: 60/084366
/ PRIOR FILING DATE: 1998-05-05
/ PRIOR APPLICATION NUMBER: 60/084414
/ PRIOR FILING DATE: 1998-05-06
/ PRIOR APPLICATION NUMBER: 60/084441
/ PRIOR FILING DATE: 1998-05-06
/ PRIOR APPLICATION NUMBER: 60/084637
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084639
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084640
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084598
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084600
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084627
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084643
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/085339
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085338
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085323
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085582
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085700
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085689
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085579
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085580
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085573
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	1.19e-41	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-978-191A-522 (1-1679)

QY	1	MetLysThrIleGlnProLysMethHisAsnSerIleSerTrpAlaIlePheThrGlyLeu	20
DB	134	ATGAACCATCCAGCAAAATGCAAAATTCCTCTTGGCAATCTTCACGGGGCTG	193
QY	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
DB	194	GCTGCTCTGTCTCTTCCAAAGGAGTCCCGTGGCAGCGGAGATGCCACCTTCCCCAAA	253
QY	41	AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
DB	254	GCTATGGACAACGTGACGTCGGCAGCGGGAGAGCGCCACCTCAGGTGCATTATTCAC	313
QY	61	AsnArgValThrArgValAlaAlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp	80

Db 314 AACGGGTGTCACCCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
Db 374 AAGTGGTGGCTGGATCTCGCGTGGTCTCTCTGAGCAACACCCAAACGAGTACAGCATC 433
Qy 101 GlutIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTGGTGCAACAGAC 493
Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCAACCAAGACCTCTAGGGTCCACCTATTGTGCAAGTATCTCCCAAAATTTGTAGAG 553
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTTCTTCAGATATCTCCATTAAAGGGGAACAATATTAGCCCTCACCCTGCATAGCAACT 613
Qy 161 GlyArgProGluProThrValThrTyrArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACCAAGACCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyThrArgGluGlnSerGlyAspTyrGlu 200
Db 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCGGAGCAGTCAGGGGACTACGAG 733
Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
Db 734 TGCAGTGCCTCCATGACGTGGCGCCGCGGTGTGAGAGATGAAGTCAACGTGAAC 793
Qy 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCCACCATACATTTCCAGAACCAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAspAspLys 260
Db 854 CTGCAGTGTGAAGCCTTCAGCAGTCCCTCCAGCAGAAATTCAGTGGTCAAGGATGACAAA 913
Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTGAAGGAAGAGGGGTGAAGTGGAAACACACACCTTCTCTCAAACTC 973
Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db 974 ATCTTCTTCAATGCTCTGAAACATGACTATGGAACTACTTGGTGGCTCCCAACAAAG 1033
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1034 CTGGCCCAACCAATGCCAGCATCATGCTATTGTGTCAGGCGCGCTCAGCGAGTGTGAGC 1093
Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340
Db 1094 AACGCGCTGAGGAGGCGAGGCTGGCTGGCTGCTGCTCTTCTGCTGTGCACTG 1153
Qy 341 LeuLeuLysPhe 344
Db 1154 CTCTCAAAATTT 1165

RESULT 10
US-09-978-403A-522
; Sequence 522, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107

1 PRIOR FILING DATE: 1998-03-31
2 PRIOR APPLICATION NUMBER: 60/080165
3 PRIOR FILING DATE: 1998-03-31
4 PRIOR APPLICATION NUMBER: 60/080194
5 PRIOR FILING DATE: 1998-03-31
6 PRIOR APPLICATION NUMBER: 60/080327
7 PRIOR FILING DATE: 1998-04-01
8 PRIOR APPLICATION NUMBER: 60/080328
9 PRIOR FILING DATE: 1998-04-01
10 PRIOR APPLICATION NUMBER: 60/080333
11 PRIOR FILING DATE: 1998-04-01
12 PRIOR APPLICATION NUMBER: 60/080334
13 PRIOR FILING DATE: 1998-04-01
14 PRIOR APPLICATION NUMBER: 60/081070
15 PRIOR FILING DATE: 1998-04-08
16 PRIOR APPLICATION NUMBER: 60/081049
17 PRIOR FILING DATE: 1998-04-08
18 PRIOR APPLICATION NUMBER: 60/081071
19 PRIOR FILING DATE: 1998-04-08
20 PRIOR APPLICATION NUMBER: 60/081195
21 PRIOR FILING DATE: 1998-04-08
22 PRIOR APPLICATION NUMBER: 60/081203
23 PRIOR FILING DATE: 1998-04-09
24 PRIOR APPLICATION NUMBER: 60/081229
25 PRIOR FILING DATE: 1998-04-09
26 PRIOR APPLICATION NUMBER: 60/081955
27 PRIOR FILING DATE: 1998-04-15
28 PRIOR APPLICATION NUMBER: 60/081817
29 PRIOR FILING DATE: 1998-04-15
30 PRIOR APPLICATION NUMBER: 60/081819
31 PRIOR FILING DATE: 1998-04-15
32 PRIOR APPLICATION NUMBER: 60/081952
33 PRIOR FILING DATE: 1998-04-15
34 PRIOR APPLICATION NUMBER: 60/081838
35 PRIOR FILING DATE: 1998-04-15
36 PRIOR APPLICATION NUMBER: 60/082568
37 PRIOR FILING DATE: 1998-04-21
38 PRIOR APPLICATION NUMBER: 60/082569
39 PRIOR FILING DATE: 1998-04-21
40 PRIOR APPLICATION NUMBER: 60/082704
41 PRIOR FILING DATE: 1998-04-22
42 PRIOR APPLICATION NUMBER: 60/082804
43 PRIOR FILING DATE: 1998-04-22
44 PRIOR APPLICATION NUMBER: 60/082700
45 PRIOR FILING DATE: 1998-04-22
46 PRIOR APPLICATION NUMBER: 60/082797
47 PRIOR FILING DATE: 1998-04-22
48 PRIOR APPLICATION NUMBER: 60/082796
49 PRIOR FILING DATE: 1998-04-23
50 PRIOR APPLICATION NUMBER: 60/083336
51 PRIOR FILING DATE: 1998-04-27
52 PRIOR APPLICATION NUMBER: 60/083322
53 PRIOR FILING DATE: 1998-04-28
54 PRIOR APPLICATION NUMBER: 60/083392
55 PRIOR FILING DATE: 1998-04-29
56 PRIOR APPLICATION NUMBER: 60/083495
57 PRIOR FILING DATE: 1998-04-29
58 PRIOR APPLICATION NUMBER: 60/083496
59 PRIOR FILING DATE: 1998-04-29
60 PRIOR APPLICATION NUMBER: 60/083499
61 PRIOR FILING DATE: 1998-04-29
62 PRIOR APPLICATION NUMBER: 60/083545
63 PRIOR FILING DATE: 1998-04-29
64 PRIOR APPLICATION NUMBER: 60/083554
65 PRIOR FILING DATE: 1998-04-29
66 PRIOR APPLICATION NUMBER: 60/083558
67 PRIOR FILING DATE: 1998-04-29
68 PRIOR APPLICATION NUMBER: 60/083559
69 PRIOR FILING DATE: 1998-04-29
70 PRIOR APPLICATION NUMBER: 60/083500
71 PRIOR FILING DATE: 1998-04-29
72 PRIOR APPLICATION NUMBER: 60/083742
73 PRIOR FILING DATE: 1998-04-30

1 PRIOR APPLICATION NUMBER: 60/084366
2 PRIOR FILING DATE: 1998-05-05
3 PRIOR APPLICATION NUMBER: 60/084414
4 PRIOR FILING DATE: 1998-05-06
5 PRIOR APPLICATION NUMBER: 60/084441
6 PRIOR FILING DATE: 1998-05-06
7 PRIOR APPLICATION NUMBER: 60/084637
8 PRIOR FILING DATE: 1998-05-07
9 PRIOR APPLICATION NUMBER: 60/084639
10 PRIOR FILING DATE: 1998-05-07
11 PRIOR APPLICATION NUMBER: 60/084640
12 PRIOR FILING DATE: 1998-05-07
13 PRIOR APPLICATION NUMBER: 60/084598
14 PRIOR FILING DATE: 1998-05-07
15 PRIOR APPLICATION NUMBER: 60/084600
16 PRIOR FILING DATE: 1998-05-07
17 PRIOR APPLICATION NUMBER: 60/084627
18 PRIOR FILING DATE: 1998-05-07
19 PRIOR APPLICATION NUMBER: 60/084643
20 PRIOR FILING DATE: 1998-05-07
21 PRIOR APPLICATION NUMBER: 60/085339
22 PRIOR FILING DATE: 1998-05-13
23 PRIOR APPLICATION NUMBER: 60/085338
24 PRIOR FILING DATE: 1998-05-13
25 PRIOR APPLICATION NUMBER: 60/085323
26 PRIOR FILING DATE: 1998-05-13
27 PRIOR APPLICATION NUMBER: 60/085582
28 PRIOR FILING DATE: 1998-05-15
29 PRIOR APPLICATION NUMBER: 60/085700
30 PRIOR FILING DATE: 1998-05-15
31 PRIOR APPLICATION NUMBER: 60/085689
32 PRIOR FILING DATE: 1998-05-15
33 PRIOR APPLICATION NUMBER: 60/085579
34 PRIOR FILING DATE: 1998-05-15
35 PRIOR APPLICATION NUMBER: 60/085580
36 PRIOR FILING DATE: 1998-05-15
37 PRIOR APPLICATION NUMBER: 60/085573
38 PRIOR FILING DATE: 1998-05-15
39 PRIOR APPLICATION NUMBER: 60/085704
40 PRIOR FILING DATE: 1998-05-15
41 PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	1,19e-41	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-978-403A-522 (1-1679)

QY	1	MetLysThrIleGlnProLysMethIleSerThrAlaIlePheThrGlyLeu	20
DB	134	ATGAATAACCATCCAGCAAAATGCACAAATCTATCTCTTGGGCAATCTTCACGGGGCTG	193
QY	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
DB	194	GCTGCTCTGTGTCTTCTCCAGAGATGCCCGCGCGAGATGCCACCTTCCCAAA	253
QY	41	AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
DB	254	GCTATGGACAACGTGACGGTCCGCGAGGGGAGAGCGCACCTCAGGTGCTATTGAC	313
QY	61	AsnArgValThrArgValAlaIleThrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp	80
DB	314	AAACCGGGTCACCCGGGTGGCTGGTAAACCGCAGCACCATCTCTATGCTGGGAATGAC	373
QY	81	LysTyrCysLeuAspProArgValValLeuLeuLeuSerAsnThrGlnThrGlnTyrSerIle	100
DB	374	AAGTGGTGGCTGGATCTCTCGCGTGGTCTCTTGAGCAACACCCAAACGCGATCAGCATC	433
QY	101	GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp	120

Db	434	GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACGAC	493
Qy	121	AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu	140
Db	494	AACCACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAGTATCTCCCAAAATGTGAG	553
Qy	141	IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr	160
Db	554	ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTTCACCTGTCATGCAACT	613
Qy	161	GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal	180
Db	614	GGTAGACCAAGACCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG	673
Qy	181	SerGluAspGluTrpLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu	200
Db	674	AGTGAAGACGAATACTTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG	733
Qy	201	CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn	220
Db	734	TGCAGTGCCTCCAAATGACGTGGCCGCCGCCCTGTGTACGGAGAGTAAAGGTCAACCGTGAAC	793
Qy	221	TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr	240
Db	794	TATCCACCATACATTTGGAAGCCACGGGTACAGGTGTCCCGCTGGGACAAAGGGGACA	853
Qy	241	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys	260
Db	854	CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGGATGACAAA	913
Qy	261	ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu	280
Db	914	AGACTGATGAAGGAAGAAAGGGGTGAAGTGAAGAACAGACCTTCTCTCTCAAAATC	973
Qy	281	IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys	300
Db	974	ATCTTCTTCAATGCTCTGAAACATGACTATCGGAATACACTTGGTGGCCTCCCAACAAG	1033
Qy	301	LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer	320
Db	1034	CTGGGCCACACCAATGCCAGCATCATGTATTGTGGTCAGCGCGCGTCAGCGAGTGAGC	1093
Qy	321	AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu	340
Db	1094	AACGGCAGTCGAGGAGGGCAGCGCTGGCTGTGGCTGTGCTCTCTGGTCTTGACCTG	1153
Qy	341	LeuLeuLysPhe	344
Db	1154	CTTCTCAAAATTT	1165

RESULT 11

US-09-978-564A-522
; Sequence 522, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Borstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kliaavin, Ivar J.

1 PRIOR APPLICATION NUMBER: 60/080328
2 PRIOR FILING DATE: 1998-04-01
3 PRIOR APPLICATION NUMBER: 60/080333
4 PRIOR FILING DATE: 1998-04-01
5 PRIOR APPLICATION NUMBER: 60/080334
6 PRIOR FILING DATE: 1998-04-01
7 PRIOR APPLICATION NUMBER: 60/081070
8 PRIOR FILING DATE: 1998-04-08
9 PRIOR APPLICATION NUMBER: 60/081049
10 PRIOR FILING DATE: 1998-04-08
11 PRIOR APPLICATION NUMBER: 60/081071
12 PRIOR FILING DATE: 1998-04-08
13 PRIOR APPLICATION NUMBER: 60/081195
14 PRIOR FILING DATE: 1998-04-08
15 PRIOR APPLICATION NUMBER: 60/081203
16 PRIOR FILING DATE: 1998-04-09
17 PRIOR APPLICATION NUMBER: 60/081229
18 PRIOR FILING DATE: 1998-04-09
19 PRIOR APPLICATION NUMBER: 60/081955
20 PRIOR FILING DATE: 1998-04-15
21 PRIOR APPLICATION NUMBER: 60/081817
22 PRIOR FILING DATE: 1998-04-15
23 PRIOR APPLICATION NUMBER: 60/081819
24 PRIOR FILING DATE: 1998-04-15
25 PRIOR APPLICATION NUMBER: 60/081952
26 PRIOR FILING DATE: 1998-04-15
27 PRIOR APPLICATION NUMBER: 60/081838
28 PRIOR FILING DATE: 1998-04-15
29 PRIOR APPLICATION NUMBER: 60/082568
30 PRIOR FILING DATE: 1998-04-21
31 PRIOR APPLICATION NUMBER: 60/082569
32 PRIOR FILING DATE: 1998-04-21
33 PRIOR APPLICATION NUMBER: 60/082704
34 PRIOR FILING DATE: 1998-04-22
35 PRIOR APPLICATION NUMBER: 60/082804
36 PRIOR FILING DATE: 1998-04-22
37 PRIOR APPLICATION NUMBER: 60/082700
38 PRIOR FILING DATE: 1998-04-22
39 PRIOR APPLICATION NUMBER: 60/082797
40 PRIOR FILING DATE: 1998-04-22
41 PRIOR APPLICATION NUMBER: 60/082796
42 PRIOR FILING DATE: 1998-04-23
43 PRIOR APPLICATION NUMBER: 60/083336
44 PRIOR FILING DATE: 1998-04-27
45 PRIOR APPLICATION NUMBER: 60/083322
46 PRIOR FILING DATE: 1998-04-28
47 PRIOR APPLICATION NUMBER: 60/083332
48 PRIOR FILING DATE: 1998-04-29
49 PRIOR APPLICATION NUMBER: 60/083495
50 PRIOR FILING DATE: 1998-04-29
51 PRIOR APPLICATION NUMBER: 60/083496
52 PRIOR FILING DATE: 1998-04-29
53 PRIOR APPLICATION NUMBER: 60/083499
54 PRIOR FILING DATE: 1998-04-29
55 PRIOR APPLICATION NUMBER: 60/083545
56 PRIOR FILING DATE: 1998-04-29
57 PRIOR APPLICATION NUMBER: 60/083554
58 PRIOR FILING DATE: 1998-04-29
59 PRIOR APPLICATION NUMBER: 60/083558
60 PRIOR FILING DATE: 1998-04-29
61 PRIOR APPLICATION NUMBER: 60/083559
62 PRIOR FILING DATE: 1998-04-29
63 PRIOR APPLICATION NUMBER: 60/083500
64 PRIOR FILING DATE: 1998-04-29
65 PRIOR APPLICATION NUMBER: 60/083742
66 PRIOR FILING DATE: 1998-04-30
67 PRIOR APPLICATION NUMBER: 60/084366
68 PRIOR FILING DATE: 1998-05-05
69 PRIOR APPLICATION NUMBER: 60/084414
70 PRIOR FILING DATE: 1998-05-06
71 PRIOR APPLICATION NUMBER: 60/084441
72 PRIOR FILING DATE: 1998-05-06
73 PRIOR APPLICATION NUMBER: 60/084637

1 PRIOR FILING DATE: 1998-05-07
2 PRIOR APPLICATION NUMBER: 60/084639
3 PRIOR FILING DATE: 1998-05-07
4 PRIOR APPLICATION NUMBER: 60/084640
5 PRIOR FILING DATE: 1998-05-07
6 PRIOR APPLICATION NUMBER: 60/084598
7 PRIOR FILING DATE: 1998-05-07
8 PRIOR APPLICATION NUMBER: 60/084600
9 PRIOR FILING DATE: 1998-05-07
10 PRIOR APPLICATION NUMBER: 60/084627
11 PRIOR FILING DATE: 1998-05-07
12 PRIOR APPLICATION NUMBER: 60/084643
13 PRIOR FILING DATE: 1998-05-07
14 PRIOR APPLICATION NUMBER: 60/085339
15 PRIOR FILING DATE: 1998-05-13
16 PRIOR APPLICATION NUMBER: 60/085338
17 PRIOR FILING DATE: 1998-05-13
18 PRIOR APPLICATION NUMBER: 60/085323
19 PRIOR FILING DATE: 1998-05-13
20 PRIOR APPLICATION NUMBER: 60/085582
21 PRIOR FILING DATE: 1998-05-15
22 PRIOR APPLICATION NUMBER: 60/085700
23 PRIOR FILING DATE: 1998-05-15
24 PRIOR APPLICATION NUMBER: 60/085689
25 PRIOR FILING DATE: 1998-05-15
26 PRIOR APPLICATION NUMBER: 60/085579
27 PRIOR FILING DATE: 1998-05-15
28 PRIOR APPLICATION NUMBER: 60/085580
29 PRIOR FILING DATE: 1998-05-15
30 PRIOR APPLICATION NUMBER: 60/085573
31 PRIOR FILING DATE: 1998-05-15
32 PRIOR APPLICATION NUMBER: 60/085704
33 PRIOR FILING DATE: 1998-05-15
34 PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	1.19e-41	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-978-564A-522 (1-1679)

QY	1	MetLysThrIleGlnProLysMethIleAsnSerIleSerTrpAlaIlePheThrGlyLeu	20
DB	134	ATGAAACCATCCAGCCAAAATGCACAAATTCATCTCTTGGGCAATCTTCACGGGGCTG	193
QY	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
DB	194	GCTGCTCTGTGTCTCTTCCACGAGTGCCCGTGGCAGCGGAGATGCCACCTTCCCAAA	253
QY	41	AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
DB	254	GCTATGGACACAGTGCAGGTCCGGCAGCGGAGAGCGCCACCTCAGGTGCATATTGAC	313
QY	61	AsnArgValThrArgValAlaIleTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp	80
DB	314	AACCGGGTCACCGGGGTGGCCCTGAAACCCAGCAGCACCCTCTATCTCTGGGAATGAC	373
QY	81	LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIle	100
DB	374	AAAGTGGTGCCTGGATCCTCGCTGCTCTTCTGAGCAACACCCCAACGAGTACAGATC	433
QY	101	GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp	120
DB	434	GAGATCCAGACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC	493
QY	121	AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu	140
DB	494	AAACCAACCAAGACCTCTTAGGGTCCACCTATTGTGCAAGATATCTCCCAAAATTTAGAG	553

```
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTACACAGAGCCTACGCTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 673
QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
Db 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCGGAGCAGCTCAGGGGCACTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
Db 734 TGCACTGCTCCATAGAGTGCGCCCGCCCGTGGTACGAGATTAAGTCAACGTGAGC 793
QY 221 TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCCACCATCATTTCCAGAACCCAAAGGTTACAGGTGTCCCGTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAspAspLys 260
Db 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCCAGCAGAAATTCAGTGTGATCAAGGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTGAAGGAAAGAGGGGTGAAGTGGAAACAGACCTTCTCTCAAACTC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACACTACTTGGCTGCCCTCCACAAAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1034 CTGGCCACACCAATGCCAGCATCATGCTATTGTGTCAGGCGCGCTCAGCGAGTGAGC 1093
QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuValHisLeu 340
Db 1094 AACGGCAGCTCGAGGAGGCGAGGCTGCGTCTGGCTGCTGCTCTCTGTGCTTGTGCACTG 1153
QY 341 LeuLeuLysPhe 344
Db 1154 CTCTCAAAATTT 1165

RESULT 12
US-09-999-833A-522
; Sequence 522, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
```

```
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
```

1 PRIOR FILING DATE: 1998-04-08
2 PRIOR APPLICATION NUMBER: 60/081049
3 PRIOR FILING DATE: 1998-04-08
4 PRIOR APPLICATION NUMBER: 60/081071
5 PRIOR FILING DATE: 1998-04-08
6 PRIOR APPLICATION NUMBER: 60/081195
7 PRIOR FILING DATE: 1998-04-08
8 PRIOR APPLICATION NUMBER: 60/081203
9 PRIOR FILING DATE: 1998-04-09
10 PRIOR APPLICATION NUMBER: 60/081229
11 PRIOR FILING DATE: 1998-04-09
12 PRIOR APPLICATION NUMBER: 60/081955
13 PRIOR FILING DATE: 1998-04-15
14 PRIOR APPLICATION NUMBER: 60/081817
15 PRIOR FILING DATE: 1998-04-15
16 PRIOR APPLICATION NUMBER: 60/081819
17 PRIOR FILING DATE: 1998-04-15
18 PRIOR APPLICATION NUMBER: 60/081952
19 PRIOR FILING DATE: 1998-04-15
20 PRIOR APPLICATION NUMBER: 60/081838
21 PRIOR FILING DATE: 1998-04-15
22 PRIOR APPLICATION NUMBER: 60/082568
23 PRIOR FILING DATE: 1998-04-21
24 PRIOR APPLICATION NUMBER: 60/082569
25 PRIOR FILING DATE: 1998-04-21
26 PRIOR APPLICATION NUMBER: 60/082704
27 PRIOR FILING DATE: 1998-04-22
28 PRIOR APPLICATION NUMBER: 60/082804
29 PRIOR FILING DATE: 1998-04-22
30 PRIOR APPLICATION NUMBER: 60/082700
31 PRIOR FILING DATE: 1998-04-22
32 PRIOR APPLICATION NUMBER: 60/082797
33 PRIOR FILING DATE: 1998-04-22
34 PRIOR APPLICATION NUMBER: 60/082796
35 PRIOR FILING DATE: 1998-04-23
36 PRIOR APPLICATION NUMBER: 60/083336
37 PRIOR FILING DATE: 1998-04-27
38 PRIOR APPLICATION NUMBER: 60/083322
39 PRIOR FILING DATE: 1998-04-28
40 PRIOR APPLICATION NUMBER: 60/083392
41 PRIOR FILING DATE: 1998-04-29
42 PRIOR APPLICATION NUMBER: 60/083495
43 PRIOR FILING DATE: 1998-04-29
44 PRIOR APPLICATION NUMBER: 60/083496
45 PRIOR FILING DATE: 1998-04-29
46 PRIOR APPLICATION NUMBER: 60/083499
47 PRIOR FILING DATE: 1998-04-29
48 PRIOR APPLICATION NUMBER: 60/083545
49 PRIOR FILING DATE: 1998-04-29
50 PRIOR APPLICATION NUMBER: 60/083554
51 PRIOR FILING DATE: 1998-04-29
52 PRIOR APPLICATION NUMBER: 60/083558
53 PRIOR FILING DATE: 1998-04-29
54 PRIOR APPLICATION NUMBER: 60/083559
55 PRIOR FILING DATE: 1998-04-29
56 PRIOR APPLICATION NUMBER: 60/083500
57 PRIOR FILING DATE: 1998-04-29
58 PRIOR APPLICATION NUMBER: 60/083742
59 PRIOR FILING DATE: 1998-04-30
60 PRIOR APPLICATION NUMBER: 60/084366
61 PRIOR FILING DATE: 1998-05-05
62 PRIOR APPLICATION NUMBER: 60/084414
63 PRIOR FILING DATE: 1998-05-06
64 PRIOR APPLICATION NUMBER: 60/084441
65 PRIOR FILING DATE: 1998-05-06
66 PRIOR APPLICATION NUMBER: 60/084637
67 PRIOR FILING DATE: 1998-05-07
68 PRIOR APPLICATION NUMBER: 60/084639
69 PRIOR FILING DATE: 1998-05-07
70 PRIOR APPLICATION NUMBER: 60/084640
71 PRIOR FILING DATE: 1998-05-07
72 PRIOR APPLICATION NUMBER: 60/084598
73 PRIOR FILING DATE: 1998-05-07

1 PRIOR APPLICATION NUMBER: 60/084600
2 PRIOR FILING DATE: 1998-05-07
3 PRIOR APPLICATION NUMBER: 60/084627
4 PRIOR FILING DATE: 1998-05-07
5 PRIOR APPLICATION NUMBER: 60/084643
6 PRIOR FILING DATE: 1998-05-07
7 PRIOR APPLICATION NUMBER: 60/085339
8 PRIOR FILING DATE: 1998-05-13
9 PRIOR APPLICATION NUMBER: 60/085338
10 PRIOR FILING DATE: 1998-05-13
11 PRIOR APPLICATION NUMBER: 60/085323
12 PRIOR FILING DATE: 1998-05-13
13 PRIOR APPLICATION NUMBER: 60/085582
14 PRIOR FILING DATE: 1998-05-15
15 PRIOR APPLICATION NUMBER: 60/085700
16 PRIOR FILING DATE: 1998-05-15
17 PRIOR APPLICATION NUMBER: 60/085689
18 PRIOR FILING DATE: 1998-05-15
19 PRIOR APPLICATION NUMBER: 60/085579
20 PRIOR FILING DATE: 1998-05-15
21 PRIOR APPLICATION NUMBER: 60/085580
22 PRIOR FILING DATE: 1998-05-15
23 PRIOR APPLICATION NUMBER: 60/085573
24 PRIOR FILING DATE: 1998-05-15
25 PRIOR APPLICATION NUMBER: 60/085704
26 PRIOR FILING DATE: 1998-05-15
27 PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 1.19e-41 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-999-833A-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMethHisAsnSerIleSerTyrAlaIlePheThrGlyLeu 20
Db 134 ATGAACCATCCAGCCAAATGCAATCTATCTCTTGGCAATCTTACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTCTCTTCCAGGAGTGCGCGCGAGGAGATGCCACCTTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCTCAGGTGCATATTGAC 313
QY 61 AsnArgValThrArgValAlaIleTyrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
Db 314 AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCACCTCTATCTCTGGGATGAC 373
QY 81 LysTyrCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
Db 374 AAGTGGTGGTGGATCCTCGCTGGTCTCTTGAGCAACACCCAAACGACGATACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAACGTGGATGTGTATCAGGAGGCCCTTACACCTGTCTGGTGAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGGCAAGTATCTCCCAAAATTTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTTCTCAGATATCTCCATTAAAGGGAACAATATTAGCTCCTACCTGCATAGCAACT 613
QY 161 GlyArgProGluProThrValThrTyrArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACCAAGCCCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673

; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339

; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 1.19e-41 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-981-915A-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMethHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB 134 ATGAARACCATCCAGCCAAATATGACAAATCTATCTCTTGGCAATCTTCACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTCTGTCTCTTCCAGGAGTGCCGTGCGCAGCGAGATGCCACCTTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGGACAACGTGACGTCCGGTCCGGCAGGGGAGAGGCCACCTCAGGTGCATATTGAC 313
QY 61 AsnArgValThrArgValAlaIleTrpLeuAsnArgSerThrIleLeuTrpAlaGlyAsnAsp 80
DB 314 AACCGGGTCCACCGGGTGGCTGGCTAAACCGCAGACCATCTCTATGCTGGGATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIle 100
DB 374 AAGTGGTGGCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTrpAspGluGlyProTrpThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAG 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCCCAAGACCTCTAGGGTCCACCTCAITGTGCAAGTATCTCCCAAAATGTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTCTCTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACCAAGACCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGG 673
QY 181 SerGluAspGluTrpLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTrpGlu 200
DB 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaIleProValValArgArgValLysValThrValAsn 220

Db 734 TGCAGTGCCTCCATGACGTGGCGCGCCCGTGGTACGAGAGTAAAGGTACCGTGAAC 793
QY 221 TyrProProTyrTilSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCACCACCATATTCAGAACCCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrTyrAspAspLys 260
Db 854 CTGCGAGTGTGAAGCTTCAGCATCCCTCCAGCAGAAATTCAGTGTGATCAAGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTAAGGAAGAAAGCGGTGAAAGTGGAAACAGACCTTTCTCTCAAAATCTC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db 974 ATCTCTTCAATGTCTCTGAACATGACTATGGGAATCACTTGGTGGCGCTCCCAACAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyValAlaValSerGluValSer 320
Db 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGTACGCGAGTGAGC 1093
QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340
Db 1094 AACGGCAGTCGAGAGGGCGAGGCTGCGTCTGGCTGTCTGCTCTCTCTGCTCTTGCACCTG 1153
QY 341 LeuLeuLysPhe 344
Db 1154 CTCTCAAAATTT 1165
RESULT 14
US-09-978-824-522
; Sequence 522, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: William, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC14
; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817

; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15

; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	1.19e-41	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-978-824-522 (1-1679)

QY	1	MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu	20
DB	134	ATGAATACCATCCAGCCAAAATATGCAATTTCTATCTCTTGGCAATCTTACGGGGCTG	193
QY	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
DB	194	GCTGCTCTGTCTCTTCCAAAGGAGTGCCCGTCCGCGAGGAGATGCCACCTTCCCAAA	253
QY	41	AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
DB	254	GCTATGGACAACGTGACCGTCCGCGAGGGGAGAGCCACCTCTAGGTGCACTATTGAC	313
QY	61	AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTrpAlaGlyAsnAsp	80
DB	314	AACCGGGTCACCCGGTGGCTGGCTAAACCGCAGCAGCACCATCTCTATGCTGGGAATGAC	373
QY	81	LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIle	100
DB	374	AAGTGGTGCTGGATCTCGCGTGGTCCCTTCTGAGCAACACCCAAACGGCAGTACAGCATC	433
QY	101	GluIleGlnAsnValAspValTyArgGlnGlyProTyThrCysSerValGlnThrAsp	120
DB	434	GAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCCCTTACACCTGCTCGGTGACAGACAG	493
QY	121	AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu	140
DB	494	AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTCAAGTATCTCCCAAAATTTGTAGAG	553
QY	141	IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr	160
DB	554	ATTCTCTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT	613
QY	161	GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal	180
DB	614	GGTAGACCAAGCCTACGGTTACTTGGAGACACATCTCTCCAAACGGTGTGCTTTGTG	673
QY	181	SerGluAspGluTyTrpLeuGlnIleGlnGlyIleThrArgGluGlnSerGlyAspTyGlu	200
DB	674	AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACATACGAG	733
QY	201	CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn	220
DB	734	TGCAGTGCCTCCAATGACGTGGCCGCGCGGTGGTACGGAGAGTAAGGTCCACCGTGAAC	793
QY	221	TyrProProTyTrpIleSerGluAlaLysGlyThrGlyValProValGlnLysGlyThr	240
DB	794	TATCCACCATATCATTTTCAGAACCAAGGTACAGGTGTCCTCCCGTGGGACAAAGGGGACA	853
QY	241	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyTrpLysAspAspLys	260


```
Db 854 CTCGAGTGTGAAGCCTCAGCAGTCCCTCCAGCAGAAATCCAGTGGTCAAGGATGACAAA 913
Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTTGAAGGAAAGAGGGGTGAAAGTGGAAACAGACCTTTCTCTCAAAATCTC 973
Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db 974 ATCTTCTTCAATGCTCTGAACATGACTATGGGAACACTACATGCTGGCCCTCCCAACAAG 1033
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGCTCAGCGAGGTGAGC 1093
Qy 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340
Db 1094 AACGGCAGCTCGAGGAGGCGAGGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCT 1153
Qy 341 LeuLeuLysPhe 344
Db 1154 CTTCTCAAAATTT 1165

RESULT 15
; Sequence 522, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C1
; CURRENT APPLICATION NUMBER: US/09/918,585A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
```

1 PRIOR APPLICATION NUMBER: 60/082569
1 PRIOR FILING DATE: 1998-04-21
1 PRIOR APPLICATION NUMBER: 60/082704
1 PRIOR FILING DATE: 1998-04-22
1 PRIOR APPLICATION NUMBER: 60/082804
1 PRIOR FILING DATE: 1998-04-22
1 PRIOR APPLICATION NUMBER: 60/082700
1 PRIOR FILING DATE: 1998-04-22
1 PRIOR APPLICATION NUMBER: 60/082797
1 PRIOR FILING DATE: 1998-04-22
1 PRIOR APPLICATION NUMBER: 60/082796
1 PRIOR FILING DATE: 1998-04-23
1 PRIOR APPLICATION NUMBER: 60/083336
1 PRIOR FILING DATE: 1998-04-27
1 PRIOR APPLICATION NUMBER: 60/083322
1 PRIOR FILING DATE: 1998-04-28
1 PRIOR APPLICATION NUMBER: 60/083392
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083495
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083496
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083499
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083545
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083554
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083558
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083559
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083500
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083742
1 PRIOR FILING DATE: 1998-04-30
1 PRIOR APPLICATION NUMBER: 60/084366
1 PRIOR FILING DATE: 1998-05-05
1 PRIOR APPLICATION NUMBER: 60/084414
1 PRIOR FILING DATE: 1998-05-06
1 PRIOR APPLICATION NUMBER: 60/084441
1 PRIOR FILING DATE: 1998-05-06
1 PRIOR APPLICATION NUMBER: 60/084637
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084639
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084640
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084598
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084600
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084627
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084643
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/085339
1 PRIOR FILING DATE: 1998-05-13
1 PRIOR APPLICATION NUMBER: 60/085338
1 PRIOR FILING DATE: 1998-05-13
1 PRIOR APPLICATION NUMBER: 60/085323
1 PRIOR FILING DATE: 1998-05-13
1 PRIOR APPLICATION NUMBER: 60/085582
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085700
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085689
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085579
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085580
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085573

1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085704
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085697
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/086023

Alignment Scores:

Pred. No.: 1,19e-41 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-017-084a-523 (1-344) x US-09-918-585A-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMethHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB 134 ATGAAACCATCCAGCCAAAATGCACAATCTATCTCTTGGCAATCTTCACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTCTGTCTCTTCCAGGAGTGCCTCGCGAGCGAGATGCCACCTTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGGACAACTGACGGTCCGGCAGGGGGAGAGCGCCACCTCAGGTGCATTGAC 313
QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
DB 314 AACCGGTCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
DB 374 AAGTGTGCTCGATCCTCGCGTGGTCTTCGAGCAACACCCAAACCGCAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCAACCAAGACCTCTAGGGTCCACCTCAATGTGCAAGTATCTCCCAAAATTTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerIleThrCysIleAlaThr 160
DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGAACAATATTAGCCTCACCTGCATAGCACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACCAAGCGCTACGGTTACTTTGGAGACACATCTCTCCCAACCGGTGGCTTTGTG 673
QY 181 SerGluAspGluTyrIleuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
DB 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCACGGGACTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaProValValArgValValLysValThrValAsn 220
DB 734 TGCAGTGCCTCCATGACGTGGCCGCCCGGTGGTACGGAGAGTAAAGGTACCGTGAAC 793
QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
DB 794 TATCCACCATACATTTTCAGAACCAAGGTGTCAGGGTGTCCCGTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIleAspAspLys 260
DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGATTCGAGTGGTACAGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
DB 914 AGACTGATTGAAGGAAGAAGGGTGAAGTGAAGGAACAGACCTTTCTCTCAAAACTC 973

QY	281	IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnIys	300	PRIOR APPLICATION NUMBER: 60/078004
				PRIOR FILING DATE: 1998-03-13
Db	974	ATCTCTTCAATGTCTCTGAACATGACATATGGAACTACATTCGGTGGCCCTCAACAAG	1033	PRIOR APPLICATION NUMBER: 60/078886
				PRIOR FILING DATE: 1998-03-20
QY	301	LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer	320	PRIOR APPLICATION NUMBER: 60/078936
				PRIOR FILING DATE: 1998-03-20
Db	1034	CTGGGCCACACCAATGCCAGCATCATGCTATTGTGTCAGGCGCGTCAGCGAGGTGAGC	1093	PRIOR APPLICATION NUMBER: 60/078910
				PRIOR FILING DATE: 1998-03-20
QY	321	AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisIeu	340	PRIOR APPLICATION NUMBER: 60/078939
				PRIOR FILING DATE: 1998-03-20
Db	1094	AACGGCACGTCGAGGAGGCGAGCTCGTCTGGCTCTTCTTGTGCTTGCACCTG	1153	PRIOR APPLICATION NUMBER: 60/079294
				PRIOR FILING DATE: 1998-03-25
QY	341	LeuLeuIlyApe 344		PRIOR APPLICATION NUMBER: 60/079656
				PRIOR FILING DATE: 1998-03-26
Db	1154	CTTCTCAATTT 1165		PRIOR APPLICATION NUMBER: 60/079664
				PRIOR FILING DATE: 1998-03-27
RESULT 16				PRIOR APPLICATION NUMBER: 60/079689
US-09-978-423A-522				PRIOR FILING DATE: 1998-03-27
Sequence 522, Application US/09978423A				PRIOR APPLICATION NUMBER: 60/079663
Publication No. US20030069178A1				PRIOR FILING DATE: 1998-03-27
GENERAL INFORMATION:				PRIOR APPLICATION NUMBER: 60/079728
APPLICANT: Ashkenazi, Avi				PRIOR FILING DATE: 1998-03-27
APPLICANT: Baker Kevin P.				PRIOR APPLICATION NUMBER: 60/079786
APPLICANT: Botstein, David				PRIOR FILING DATE: 1998-03-27
APPLICANT: Desnoyers, Luc				PRIOR APPLICATION NUMBER: 60/079920
APPLICANT: Eaton, Dan				PRIOR FILING DATE: 1998-03-30
APPLICANT: Ferrara, Napoleon				PRIOR APPLICATION NUMBER: 60/079923
APPLICANT: Filvaroff, Ellen				PRIOR FILING DATE: 1998-03-30
APPLICANT: Fong, Sherman				PRIOR APPLICATION NUMBER: 60/080105
APPLICANT: Gao, Wei-Qiang				PRIOR FILING DATE: 1998-03-31
APPLICANT: Gerber, Hanspeter				PRIOR APPLICATION NUMBER: 60/080107
APPLICANT: Gerritsen, Mary E.				PRIOR FILING DATE: 1998-03-31
APPLICANT: Goddard, Audrey				PRIOR APPLICATION NUMBER: 60/080165
APPLICANT: Godowski, Paul J.				PRIOR FILING DATE: 1998-03-31
APPLICANT: Grimaldi, J. Christopher				PRIOR APPLICATION NUMBER: 60/080194
APPLICANT: Gurney, Austin L.				PRIOR FILING DATE: 1998-03-31
APPLICANT: Hillan, Kenneth J.				PRIOR APPLICATION NUMBER: 60/080327
APPLICANT: Kijavlin, Ivar J.				PRIOR FILING DATE: 1998-04-01
APPLICANT: Kuo, Sophia S.				PRIOR APPLICATION NUMBER: 60/080328
APPLICANT: Napier, Mary A.				PRIOR FILING DATE: 1998-04-01
APPLICANT: Pan, James;				PRIOR APPLICATION NUMBER: 60/080333
APPLICANT: Paoni, Nicholas F.				PRIOR FILING DATE: 1998-04-01
APPLICANT: Roy, Margaret Ann				PRIOR APPLICATION NUMBER: 60/080334
APPLICANT: Shelton, David L.				PRIOR FILING DATE: 1998-04-01
APPLICANT: Stewart, Timothy A.				PRIOR APPLICATION NUMBER: 60/081070
APPLICANT: Tumas, Daniel				PRIOR FILING DATE: 1998-04-08
APPLICANT: Williams, P. Mickey				PRIOR APPLICATION NUMBER: 60/081049
APPLICANT: Wood, William I.				PRIOR FILING DATE: 1998-04-08
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic				PRIOR APPLICATION NUMBER: 60/081071
Acids Encoding the Same				PRIOR FILING DATE: 1998-04-08
FILE REFERENCE: P2630P1C21				PRIOR APPLICATION NUMBER: 60/081195
CURRENT APPLICATION NUMBER: US/09/978,423A				PRIOR FILING DATE: 1998-04-15
CURRENT FILING DATE: 2002-05-16				PRIOR APPLICATION NUMBER: 60/081817
PRIOR APPLICATION NUMBER: 09/918585				PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 2001-07-30				PRIOR APPLICATION NUMBER: 60/081819
PRIOR APPLICATION NUMBER: 60/062250				PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1997				

1 PRIOR FILING DATE: 1998-04-22
1 PRIOR APPLICATION NUMBER: 60/082700
1 PRIOR FILING DATE: 1998-04-22
1 PRIOR APPLICATION NUMBER: 60/082797
1 PRIOR FILING DATE: 1998-04-22
1 PRIOR APPLICATION NUMBER: 60/082796
1 PRIOR FILING DATE: 1998-04-23
1 PRIOR APPLICATION NUMBER: 60/083336
1 PRIOR FILING DATE: 1998-04-27
1 PRIOR APPLICATION NUMBER: 60/083322
1 PRIOR FILING DATE: 1998-04-28
1 PRIOR APPLICATION NUMBER: 60/083392
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083495
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083496
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083499
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083545
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083554
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083558
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083559
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083500
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083742
1 PRIOR FILING DATE: 1998-04-30
1 PRIOR APPLICATION NUMBER: 60/084366
1 PRIOR FILING DATE: 1998-05-05
1 PRIOR APPLICATION NUMBER: 60/084414
1 PRIOR FILING DATE: 1998-05-06
1 PRIOR APPLICATION NUMBER: 60/084441
1 PRIOR FILING DATE: 1998-05-06
1 PRIOR APPLICATION NUMBER: 60/084637
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084639
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084640
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084643
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/085339
1 PRIOR FILING DATE: 1998-05-13
1 PRIOR APPLICATION NUMBER: 60/085338
1 PRIOR FILING DATE: 1998-05-13
1 PRIOR APPLICATION NUMBER: 60/085323
1 PRIOR FILING DATE: 1998-05-13
1 PRIOR APPLICATION NUMBER: 60/085582
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085700
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085689
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085579
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085580
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085573
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085704
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	1.19e-41	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-978-423A-522 (1-1679)

QY	1	MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu	20
DB	134	ATGAAACCATCCAGCCAAATATGCAATTTCTATCTCTGGCAATCTTCACGGGGCTG	193
QY	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
DB	194	GCTGCTCTGTGCTCTTCCAAAGGAGTGCCTGGCGAGCGGAGATGCCACCTTCCCCAAA	253
QY	41	AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
DB	254	GCTATGGACACGTGACCGGTCCGGCAGGGGAGAGCGCCACCTTCAGGTGCATTTGAC	313
QY	61	AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp	80
DB	314	AACCGGTCACCGGGTGGCTGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC	373
QY	81	LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle	100
DB	374	AAGTGGTGCCTGGATCCTCGCGGTGCTCTTCTGAGCAACACCCAAACGCGTACAGCATC	433
QY	101	GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp	120
DB	434	GAGATCCAGACGTGGATGTGTATCAGGAGGCGCTTACACCTGCTCGGTGCAGACAGAC	493
QY	121	AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu	140
DB	494	AACCCACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCCAAAATTTGAGAG	553
QY	141	IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr	160
DB	554	ATTTCTTCAGATATCTCCATTAAAGGGAAACAATATTAGCCTCACCTGTCATAGCACT	613
QY	161	GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal	180
DB	614	GGTAGACACGACCTACCGTTACTTTGGAGACACATCTCTCCCAAGCGGTTGGCTTTGTG	673
QY	181	SerGluAspGluTyrIleuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu	200
DB	674	ACTGAAGACGAATACTTGGAAATTCAGGGGCATCACCCGGGAGCAGTCCAGGGGACTACGAG	733
QY	201	CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn	220
DB	734	TGCAGTGCCTCCATGACGTGGCCCGGCCGTGGTACGGAGAGTAAAGGTCAACGTTGAC	793
QY	221	TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr	240
DB	794	TATCCACCATACATTTCCAGAGCCAAAGGTACAGGTGTCCCGTGGGACAAAGGGGACA	853
QY	241	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIleAspAspLys	260
DB	854	CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA	913
QY	261	ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu	280
DB	914	AGACTGATTGAAGGAAGAAAGAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAACTC	973
QY	281	IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys	300
DB	974	ATCTTCTTCAATGTCTCTGNAACATCAGTATGGAACATACACTTGGCGCTCCCAACAG	1033
QY	301	LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer	320
DB	1034	CTGGGCCACACCAATGCCAGCATCATGCTATTGTTGGTCCAGGCGCGCTCAGCGAGGTGAC	1093


```

; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

US-10-017-084a-523 (1-344) x US-09-978-193A-522 (1-1679)
QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB 134 ATGAAACCATCCAGCCAAAATGCAAAATCTATCTCTTGGGCAATCTTACCGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTCTGTGTCTCTTCAAGGAGTGCCTGCGGAGGAGATGCGGAGATGCCACCTTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGGACAACTGACCGTCCGGCAGGGGAGAGGCCACCTCAGGTGACATATGAC 313
QY 61 AsnArgValThrArgValAlaIleTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp 80
DB 314 AACCGGTCACCGGGTGGCTGGCTAAACCGCAGCAGCATCTCTATGCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIle 100
DB 374 AAGTGTGCTGGATCCTCGGCTGGTCTCTTGTGACAAACACCCCAACGAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyArgGluGlyProTyThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAACGCTGATGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCAACCAAGACCTCTAGGCTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTCTTCAGATATCTCCATTAATGAGGAGAACATATTAGCTCCTCCTGCTAGCAACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACCAGAGCTACGTTTACTTTGGAGACACATCTCTCCCAAGCGTTTGGCTTTGTG 673
QY 181 SerGluAspGluTyThrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyThr 200
DB 674 AGTGAAGACGAATACTTTGAAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValValValValValVal 220
DB 734 TGCAGTGTCTCCATGACGTGGCCGCGCGCTGGTACGAGAGTAAAGGTACACCTGAC 793
QY 221 TyrProTyThrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
DB 794 TATCCACCACATATTCAGAACCCAAAGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyThrIleAspLeu 260
DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTAAGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
DB 914 AGACTGATTGAAGGAAAGAGAGGGGTGAAGTGGAAACAGACACCTTCTCTCAAAATC 973
QY 281 IlePhePheAsnValSerGluHisAspTyThrGlyAsnTyThrCysValAlaSerAsnLys 300
DB 974 ATCTTCTTCAATGTCTCTGAAATGACATGACTATGGAACTACATTTGGTGGCTCCCAACAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
DB 1034 CTGGGCCACACCAATGCCAGCATCATGTATTGTGTCAGGCGCGCTCAGGAGGTGAGC 1093
QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
DB 1094 AACGGCAGCTCAGAGGAGGGCAGGCTGGCTGTGGCTGTGCTCTTCTTCTGCTTGCACCTG 1153
QY 341 LeuLeuLysPhe 344
DB 1153

```

```

Alignment Scores:
Pred. No.: 1,19e-41
Score: 2408.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 10
Length: 1679
Matches: 344
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

```

Db 1154 CTTCTCAATT 1165

RESULT 18

US-09-999-830A-522

Sequence 522, Application US/09999830A

Publication No. US2003007700A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnovers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audtey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austan L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2630P1C70

CURRENT APPLICATION NUMBER: US/09/999,830A

CURRENT FILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077649

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791

PRIOR FILING DATE: 1998-03-12

PRIOR APPLICATION NUMBER: 60/078004

PRIOR FILING DATE: 1998-03-13

PRIOR APPLICATION NUMBER: 60/078886

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/078936

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/078939

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079294

PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/079656

PRIOR FILING DATE: 1998-03-26

PRIOR APPLICATION NUMBER: 60/079664

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/079689

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/079663

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/079728

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/079786

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/079920

PRIOR FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: 60/079923

PRIOR FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: 60/080105

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/080107

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/080165

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/080194

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/080327

PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/080328

PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/080333

PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/080334

PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/081070

PRIOR FILING DATE: 1998-04-08

PRIOR APPLICATION NUMBER: 60/081049

PRIOR FILING DATE: 1998-04-08

PRIOR APPLICATION NUMBER: 60/081071

PRIOR FILING DATE: 1998-04-08

PRIOR APPLICATION NUMBER: 60/081195

PRIOR FILING DATE: 1998-04-08

PRIOR APPLICATION NUMBER: 60/081203

PRIOR FILING DATE: 1998-04-09

PRIOR APPLICATION NUMBER: 60/081229

PRIOR FILING DATE: 1998-04-09

PRIOR APPLICATION NUMBER: 60/081955

PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER: 60/081817

PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER: 60/081819

PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER: 60/081952

PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER: 60/081838

PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER: 60/082568

PRIOR FILING DATE: 1998-04-21

PRIOR APPLICATION NUMBER: 60/082569

PRIOR FILING DATE: 1998-04-21

PRIOR APPLICATION NUMBER: 60/082704

PRIOR FILING DATE: 1998-04-22

PRIOR APPLICATION NUMBER: 60/082804

PRIOR FILING DATE: 1998-04-22

PRIOR APPLICATION NUMBER: 60/082700

PRIOR FILING DATE: 1998-04-22

PRIOR APPLICATION NUMBER: 60/082797

PRIOR FILING DATE: 1998-04-22

PRIOR APPLICATION NUMBER: 60/082796

PRIOR FILING DATE: 1998-04-23

PRIOR APPLICATION NUMBER: 60/083336

PRIOR FILING DATE: 1998-04-27

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/083392

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083495

1 PRIOR FILING DATE: 1998-04-29
2 PRIOR APPLICATION NUMBER: 60/083496
3 PRIOR FILING DATE: 1998-04-29
4 PRIOR APPLICATION NUMBER: 60/083499
5 PRIOR FILING DATE: 1998-04-29
6 PRIOR APPLICATION NUMBER: 60/083545
7 PRIOR FILING DATE: 1998-04-29
8 PRIOR APPLICATION NUMBER: 60/083554
9 PRIOR FILING DATE: 1998-04-29
10 PRIOR APPLICATION NUMBER: 60/083558
11 PRIOR FILING DATE: 1998-04-29
12 PRIOR APPLICATION NUMBER: 60/083559
13 PRIOR FILING DATE: 1998-04-29
14 PRIOR APPLICATION NUMBER: 60/083500
15 PRIOR FILING DATE: 1998-04-29
16 PRIOR APPLICATION NUMBER: 60/083742
17 PRIOR FILING DATE: 1998-04-30
18 PRIOR APPLICATION NUMBER: 60/084366
19 PRIOR FILING DATE: 1998-05-05
20 PRIOR APPLICATION NUMBER: 60/084414
21 PRIOR FILING DATE: 1998-05-06
22 PRIOR APPLICATION NUMBER: 60/084441
23 PRIOR FILING DATE: 1998-05-06
24 PRIOR APPLICATION NUMBER: 60/084637
25 PRIOR FILING DATE: 1998-05-07
26 PRIOR APPLICATION NUMBER: 60/084639
27 PRIOR FILING DATE: 1998-05-07
28 PRIOR APPLICATION NUMBER: 60/084640
29 PRIOR FILING DATE: 1998-05-07
30 PRIOR APPLICATION NUMBER: 60/084598
31 PRIOR FILING DATE: 1998-05-07
32 PRIOR APPLICATION NUMBER: 60/084600
33 PRIOR FILING DATE: 1998-05-07
34 PRIOR APPLICATION NUMBER: 60/084627
35 PRIOR FILING DATE: 1998-05-07
36 PRIOR APPLICATION NUMBER: 60/084643
37 PRIOR FILING DATE: 1998-05-07
38 PRIOR APPLICATION NUMBER: 60/085339
39 PRIOR FILING DATE: 1998-05-13
40 PRIOR APPLICATION NUMBER: 60/085338
41 PRIOR FILING DATE: 1998-05-13
42 PRIOR APPLICATION NUMBER: 60/085323
43 PRIOR FILING DATE: 1998-05-13
44 PRIOR APPLICATION NUMBER: 60/085582
45 PRIOR FILING DATE: 1998-05-15
46 PRIOR APPLICATION NUMBER: 60/085700
47 PRIOR FILING DATE: 1998-05-15
48 PRIOR APPLICATION NUMBER: 60/085689
49 PRIOR FILING DATE: 1998-05-15
50 PRIOR APPLICATION NUMBER: 60/085579
51 PRIOR FILING DATE: 1998-05-15
52 PRIOR APPLICATION NUMBER: 60/085580
53 PRIOR FILING DATE: 1998-05-15
54 PRIOR APPLICATION NUMBER: 60/085573
55 PRIOR FILING DATE: 1998-05-15
56 PRIOR APPLICATION NUMBER: 60/085704
57 PRIOR FILING DATE: 1998-05-15
58 PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 1,19e-41
Score: 2408.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 10

Length: 1679
Matches: 344
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-017-084a-523 (1-344) x US-09-999-830A-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB 134 ATGAAACCACTCCAGCCAAATGCAATCTCTCTTGGGCAATCTTACGGGGCTG 193

QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTCTGTGTCTCTTCAAGGAGTGCCTGCGGAGCGGAGATGCCACCTTCCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGGACAACGTCAGCTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 313
QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
DB 314 AACCGGTCACCGGGTGGCTGAAACCGCAGCAGCACCATCTCTATCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
DB 374 AAGTGGTGCCTGGATCCTCGCTGGTCTTCTGAGCAACCCCAACGCGGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAAGCTGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisIleuValGlnValSerProLysIleValGlu 140
DB 494 AACCAACCCAAAGACCTTAGGGTCCACCTCATTTGTCAAGTATCTCCCAAAATTGTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTTCTTCAGATATCTCCATTAATGAGGGAACAATATTAGCTCACCCTGATAGCACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACCAAGACCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
QY 181 SerGluAspGluTyrIleuGlnIleThrArgGluGlnSerGlyAspTyrGlu 200
DB 674 AGTGAAGACGAATACTTGGAAATTCAGGCAATCCCGGAGCAGTCACGGGACATACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaProValValArgArgValLysValThrValAsn 220
DB 734 TGCAGTGCCTCAATGACGTGGCCGCGCCGCTGGTACGGAGAGTAAGGTCCACCGTAAC 793
QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
DB 794 TATCCACCATACATTTCAAGCCAAAGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspLys 260
DB 854 CTGCAGTGAAGCCTTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
DB 914 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAACACAGACCTTCTCTCNAAACTC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
DB 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAATACACTTGGGTGGCTCCACCAAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyValAlaValSerGluValSer 320
DB 1034 CTGGCCACACCAATGCCAGCATCATGTATTGGTCCAGGCGCGCTCAGCGAGGTAGC 1093

321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
DB 1094 AACGGCACGTCGAGGAGGCGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1153
QY 341 LeuLeuLysPhe 344
DB 1154 CTCTCAAATTT 1165

RESULT 19

US-09-978-757A-522
; Sequence 522, Application US/09978757A
; Publication No. US20030083248A1
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC26
CURRENT APPLICATION NUMBER: US/09/978,757A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29

```
/ PRIOR APPLICATION NUMBER: 60/083554
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083558
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083559
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083500
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083742
/ PRIOR FILING DATE: 1998-04-30
/ PRIOR APPLICATION NUMBER: 60/084366
/ PRIOR FILING DATE: 1998-05-05
/ PRIOR APPLICATION NUMBER: 60/084414
/ PRIOR FILING DATE: 1998-05-06
/ PRIOR APPLICATION NUMBER: 60/084441
/ PRIOR FILING DATE: 1998-05-06
/ PRIOR APPLICATION NUMBER: 60/084637
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084639
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084640
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084598
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084600
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084627
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084643
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/085339
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085338
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085323
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085582
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085700
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085689
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085579
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085580
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085573
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697
```

Alignment Scores:

```
Pred. No.: 1,19e-41 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
```

US-10-017-084A-523 (1-344) x US-09-978-757A-522 (1-1679)

```
QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB 134 ATGAAACCATCCAGCCAAATGCAATTTCTATCTCTTGGCAATCTTCAGGGGCTG 193
QY 21 AlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTCTGTCTCTTCCAAAGAGTGCCGTCGCGAGGGAGATGCCACCTTCCCAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrIleuArgCysThrIleAsp 60
DB 254 GCTATGGACAACGTGACGTCGGGTCGGGAGAGAGGCCACCCCTCAGGTGCATTGAC 313
```

RESULT 20

```
US-09-978-187B-522
; Sequence 522, Application US/09978187B
; Publication No. US20030096744A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
```

```
QY 61 AsnArgValThrArgValAlaIleTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp 80
DB 314 AACCGGGTCACCGGGTGGCGCTGAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIle 100
DB 374 AAGTGGTGGCTGGATCTCTCGGGTGGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTrpAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAACGTCGATGTGTATGACGAGGCGCCTTACACCTGCTCGGTGAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGCAAGTATCTCCCAAAATTGTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTCTTCAGATATCTCCATTAAATGAAGGAAACAATATTAGCCTCACCTGCATAGCAACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACCAAGCCCTACCGTTTACTTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 673
QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
DB 674 AGTGAAGACGAATCTTGGAAATTCAGGGCATACCCGGGAGCAGTCAAGGGCATACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValLysValThrValAsn 220
DB 734 TGCAGTGCCTCCAATGACGTGCGCGCGCGCTGGGTACGAGAGTAAAGSTCACCGTGAAC 793
QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
DB 794 TATCCACCATATCTTTCAGAAAGCCAAAGGTTACAGGTGTCCCGGTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIleAspAspLys 260
DB 854 CTGCAGTGTGAAGCCCTCAGCAGTCCCTCCAGAGAAATTCACAGTGTGTACAGGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
DB 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAACACAGACCTTTCTCTCAAAACTC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnThrCysValAlaSerAsnLys 300
DB 974 ATCTTCTTCAATGTCTCTGAAACATGACTATGGAACTACACTTGCCTGCGCTCCAAACAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
DB 1034 CTGGSCCAACCATGCCAGCATCATGTATTTGGTCCAGGGCGCTCAGCGAGGTGAGC 1093
QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
DB 1094 AACGGCAGCTCAGGAGGAGGAGGCTGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
QY 341 LeuLeuLysPhe 344
DB 1154 CTCTCAAAATTT 1165
```

; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC5
; CURRENT APPLICATION NUMBER: US/09/978,187B
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/065364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500

; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083742
 ; PRIOR FILING DATE: 1998-04-30
 ; PRIOR APPLICATION NUMBER: 60/084366
 ; PRIOR FILING DATE: 1998-05-05
 ; PRIOR APPLICATION NUMBER: 60/084414
 ; PRIOR FILING DATE: 1998-05-06
 ; PRIOR APPLICATION NUMBER: 60/084441
 ; PRIOR FILING DATE: 1998-05-06
 ; PRIOR APPLICATION NUMBER: 60/084637
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084639
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084640
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084598
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084600
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084627
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084643
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/085339
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085338
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085323
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085582
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085700
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085689
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
 Pred. No.: 1,19e-41
 Score: 2408.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 10

US-10-017-084a-523 (1-344) x US-09-978-187B-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAAACCATCCAGCAAAATGCAATTTCTATCTCTGGGCAATCTTCACGGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTCTGTCTCTTCAAGAGAGTCCCGCGCAGCGGAGATGCCACCTTCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 DB 254 GCTATGACACACTGACGCTCCGCGAGGGGAGAGCCACCTCAGGTGACATATGAC 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyraAlaGlyAsnAsp 80
 DB 314 AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCACCATCTCTATGCTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnThrSerIle 100

DB 374 AAGTGGTGGCTGGATCTCGGTGGTCTCTCTGAGCAACACCCACCCAGTACAGCATC 433
 QY 101 GluIleGlnAsnValAspValTyraAspGluGlyProTyThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACACCCCAAGACCTTAGGGTCCACCTCATTTGGCAAGATATCTCCCAAAATTGTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTTCTTCAGATATCTCCATTAAAGGAACAATATTAGCCTCACCTGCATAGCAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACCAGACCTTACCGTTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
 QY 181 SerGluAspGluTyThrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyThr 200
 DB 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValValValValValValAsn 220
 DB 734 TGCAGTGGCTTCCAATGACGTGGCGCGCCGTGGTACGAGAGTAAAGGTCAACCGTGAAC 793
 QY 221 TyrProProTyThrIleSerGluAlaGlyGlyThrGlyValProValGlyGlyGlyThr 240
 DB 794 TATCCACCATACATTTCAAGAGCCAAAGGGTACAGGTGTCCCGGTGGGACAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyThrLysAspLys 260
 DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 DB 914 AGACTGATTGAAGGAAAGAGGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 973
 QY 281 IlePhePheAsnValSerGluHisAspTyThrGlyAsnTyThrCysValAlaSerAsnLys 300
 DB 974 ATCTTCTTCAATGTCTCTGAACATGACATATGGAAGTGAAGTGAAGTGAAGTGAAGT 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGGCCACACCAATGCCAGCATCATGTATTTGGTCCAGCGCGCTCAGCGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisIle 340
 DB 1094 AACGGCAGCTCGAGGAGGGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
 QY 341 LeuLeuLysPhe 344
 DB 1154 CTCTCAAAATTT 1165

RESULT 21
 US-09-978-643A-522
 ; Sequence 522, Application US/09978643A
 ; Publication No. US20030104998A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher

```

; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C16
; CURRENT APPLICATION NUMBER: US/09/978,643A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-978-643A-522

Alignment Scores:
Pred. No.: 1,19e-41 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-017-084a-523 (1-344) x US-09-978-643A-522 (1-1679)

Qy 1 MetLysThrLeuGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
Db 134 ATGAAACCACTCCAGCCAAATATCTATCTCTTGGGCAATCTTCACGGGGCTG 193
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTGTCCTTCCAAAGGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCCAAA 253
Qy 41 AlaMetAspAsnValThrValArgGlnGlyCysLeuSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGACACACGTCGCGTCCGCGAGGGGAGAGCCACCTCAGTGCATATTGAC 313
Qy 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrrAlaGlyAsnAsp 80
Db 314 AACCGGTTCACCGGGTGGCTGTAAACCGCAGCACCATCTCTTATGCTGGGAATGAC 373
Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrrSerIle 100
Db 374 AAGTGGTGCTGGATCTCTCGCTGGTCTTCTGAGCAACACCCAAACGCGATCAGCATC 433
Qy 101 GluIleGlnAsnValAspValTyrrAspGluGlyProTyrrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGACGTCGATGTATGACGAGGGCCCTTACACCTCTCGTGGCAGACAGAC 493
Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCAACCAAGACCTCTAGGGTCCACTCTATTTGGCAAGATATCTCCCAAAATTTGTAGAG 553
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysAlaAlaThr 160
Db 554 ATTTCTTCAGATATCTCAATTAAGAGGGGAACATATTAGCCTCAGCTGGATAGCAACT 613
Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACCAAGACCTTACGTTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
Qy 181 SerGluAspGluTyrrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrrGlu 200

```

```

674 AGTGAAGACGATACCTTGGAAATTCAGGSCATCACCAGGAGCAGTCAAGGAGCTACAGAG 733
Db
201 CysSerAlaSerAsnAspValAlaIaProValValArgValArgValValValValAsn 220
Db
734 TGCAGTGCCTCCAAATGACGTCGCGCGCGCTGTTACGGAGAGTAAAGGTCACCGTGAAC 793
Qy
221 TyrProProTyrrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db
794 TATCCACCATACATTTCAAGAGCCAAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
Qy
241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrrLysAspAspLys 260
Db
854 CTGCACTGTGAGGCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGGATGACAAA 913
Qy
261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db
914 AGACTGATTTGAAGGAAAGAAAGGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 973
Qy
281 IlePhePheAsnValSerGluHisAspTyrrGlyAsnTyrrThrCysValAlaSerAsnLys 300
Db
974 ATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGCCTGCTCCCAACAG 1033
Qy
301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyValAlaValSerGluValSer 320
Db
1034 CTGGGCCACACCAATGCCAGCATCATGCTATTGTTGTCAGGCGCGCTCAGCGAGGTGAGC 1093
Qy
321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
Db
1094 AACGGCACCTCGAGGAGGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
Qy
341 LeuLeuLysPhe 344
Db
1154 CTTCACAAATTT 1165

RESULT 22
US-09-978-375A-522
; Sequence 522, Application US/09978375A
; Publication No. US20030130181A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C24
; CURRENT APPLICATION NUMBER: US/09/978,375A
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm

```

; NUMBER OF SEQ ID NOS: 624

; SEQ ID NO 522

; LENGTH: 1679

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-978-375A-522

Alignment Scores:

Pred. No.: 1,19e-41 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-375A-522 (1-1679)

```
QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB 134 ATGAAACCATCCAGCCAAATGCAATTTCTATCTTTGGCAATCTTCACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTCTGTGCTCTTCCAAAGAGTGCCTGCGCAGCGAGATGCCACCTTCGCCCAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGGACAACTGACGGTCCGGCAGGGGAGAGGCCACCTCAGGTGCACTATTGAC 313
QY 61 AsnArgValThrArgValAlaIleTrpLeuAsnArgSerThrIleLeuTrpAlaGlyAsnAsp 80
DB 314 AACCGGGTCACCGGGTGGCTGGCTAAACCCGACGACCATCTCTATCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIle 100
DB 374 AAGTGGTGGCTGGATCTCGCTGGTCTCTTGAGCAACCCAAACGCGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTrpAspGluGlyProTrpThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAG 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCCACCAAGACCTCTAGGTGTCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTTCTTCAGATATCTCCATTAATGAGGAGACATATTAGCTTACCTGCAATAGCACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACCAAGAGCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
QY 181 SerGluAspGluTrpLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTrpGlu 200
DB 674 AGTGAAGACGAATCTTGAATATTCAGGGCATCACCCGGGAGCGTFCAGGGGACATCAG 733
QY 201 CysSerAlaSerAsnAspValAlaProValValArgValLysValThrValAsn 220
DB 734 TGCAGTGGCTTCCATGACCTGGCCGGCCGGTGTGTACGAGAGTAAGGTCCACCGTGAAC 793
QY 221 TyrProTrpTrpIleSerGluAlaLysGlyThrGlyValProValGlnGlnLysGlyThr 240
DB 794 TATCCACCATATCTTCAAGCAAGGCTACAGGTGTCTCCCGTGGGCAAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTrpLysAspAspLys 260
DB 854 CTGCAGTGTGAAGCTTCAGCAGTCCCTCAGCAGATTCAGTGTGTACAGGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
DB 914 AGACTGATTTGAAGAAAGAGGGTGAAGGTGAAGGTGAAGAGACACCTTCTCTCAAAACTC 973
```

RESULT 23

US-09-978-298A-522

; Sequence 522, Application US/09978298A

; Publication No. US20030134785A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C2

; CURRENT APPLICATION NUMBER: US/09/978,298A

; PRIOR FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: 60/077450

; PRIOR FILING DATE: 1998-03-10

; PRIOR APPLICATION NUMBER: 60/077632

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077641

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077791

; PRIOR FILING DATE: 1998-03-12

```
QY 281 IlePhePheAsnValSerGluHisAspTrpGlyAsnTrpThrCysValAlaSerAsnLys 300
DB 974 ATCTTCTTCATGCTCTGAACATGACTATGGAACTACACTTGGGTGGCTTCCACAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
DB 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTATTGGTCAGGCGCGCTCAGCGAGGTGAGC 1093
QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuProLeuValLeuHisLeu 340
DB 1094 AACGGCAGCTGAGGAGGGCAGGCTGCTCTGGCTGCTGCTCTTCTTGTGCTTGCACCTG 1153
QY 341 LeuLeuLysPhe 344
DB 1154 CTTCTCAATTT 1165
```


1 PRIOR APPLICATION NUMBER: 60/078004
2 PRIOR FILING DATE: 1998-03-13
3 PRIOR APPLICATION NUMBER: 60/078886
4 PRIOR FILING DATE: 1998-03-20
5 PRIOR APPLICATION NUMBER: 60/078936
6 PRIOR FILING DATE: 1998-03-20
7 PRIOR APPLICATION NUMBER: 60/078910
8 PRIOR FILING DATE: 1998-03-20
9 PRIOR APPLICATION NUMBER: 60/078939
10 PRIOR FILING DATE: 1998-03-20
11 PRIOR APPLICATION NUMBER: 60/079294
12 PRIOR FILING DATE: 1998-03-25
13 PRIOR APPLICATION NUMBER: 60/079656
14 PRIOR FILING DATE: 1998-03-26
15 PRIOR APPLICATION NUMBER: 60/079664
16 PRIOR FILING DATE: 1998-03-27
17 PRIOR APPLICATION NUMBER: 60/079689
18 PRIOR FILING DATE: 1998-03-27
19 PRIOR APPLICATION NUMBER: 60/079663
20 PRIOR FILING DATE: 1998-03-27
21 PRIOR APPLICATION NUMBER: 60/079728
22 PRIOR FILING DATE: 1998-03-27
23 PRIOR APPLICATION NUMBER: 60/079786
24 PRIOR FILING DATE: 1998-03-27
25 PRIOR APPLICATION NUMBER: 60/079920
26 PRIOR FILING DATE: 1998-03-30
27 PRIOR APPLICATION NUMBER: 60/079923
28 PRIOR FILING DATE: 1998-03-30
29 PRIOR APPLICATION NUMBER: 60/080105
30 PRIOR FILING DATE: 1998-03-31
31 PRIOR APPLICATION NUMBER: 60/080107
32 PRIOR FILING DATE: 1998-03-31
33 PRIOR APPLICATION NUMBER: 60/080165
34 PRIOR FILING DATE: 1998-03-31
35 PRIOR APPLICATION NUMBER: 60/080194
36 PRIOR FILING DATE: 1998-03-31
37 PRIOR APPLICATION NUMBER: 60/080327
38 PRIOR FILING DATE: 1998-04-01
39 PRIOR APPLICATION NUMBER: 60/080328
40 PRIOR FILING DATE: 1998-04-01
41 PRIOR APPLICATION NUMBER: 60/080333
42 PRIOR FILING DATE: 1998-04-01
43 PRIOR APPLICATION NUMBER: 60/080334
44 PRIOR FILING DATE: 1998-04-01
45 PRIOR APPLICATION NUMBER: 60/081070
46 PRIOR FILING DATE: 1998-04-08
47 PRIOR APPLICATION NUMBER: 60/081049
48 PRIOR FILING DATE: 1998-04-08
49 PRIOR APPLICATION NUMBER: 60/081071
50 PRIOR FILING DATE: 1998-04-08
51 PRIOR APPLICATION NUMBER: 60/081195
52 PRIOR FILING DATE: 1998-04-08
53 PRIOR APPLICATION NUMBER: 60/081203
54 PRIOR FILING DATE: 1998-04-09
55 PRIOR APPLICATION NUMBER: 60/081229
56 PRIOR FILING DATE: 1998-04-09
57 PRIOR APPLICATION NUMBER: 60/081955
58 PRIOR FILING DATE: 1998-04-15
59 PRIOR APPLICATION NUMBER: 60/081817
60 PRIOR FILING DATE: 1998-04-15
61 PRIOR APPLICATION NUMBER: 60/081819
62 PRIOR FILING DATE: 1998-04-15
63 PRIOR APPLICATION NUMBER: 60/081952
64 PRIOR FILING DATE: 1998-04-15
65 PRIOR APPLICATION NUMBER: 60/081838
66 PRIOR FILING DATE: 1998-04-15
67 PRIOR APPLICATION NUMBER: 60/082568
68 PRIOR FILING DATE: 1998-04-21
69 PRIOR APPLICATION NUMBER: 60/082569
70 PRIOR FILING DATE: 1998-04-21
71 PRIOR APPLICATION NUMBER: 60/082704
72 PRIOR FILING DATE: 1998-04-22
73 PRIOR APPLICATION NUMBER: 60/082804

74 PRIOR FILING DATE: 1998-04-22
75 PRIOR APPLICATION NUMBER: 60/082700
76 PRIOR FILING DATE: 1998-04-22
77 PRIOR APPLICATION NUMBER: 60/082797
78 PRIOR FILING DATE: 1998-04-22
79 PRIOR APPLICATION NUMBER: 60/082796
80 PRIOR FILING DATE: 1998-04-23
81 PRIOR APPLICATION NUMBER: 60/083336
82 PRIOR FILING DATE: 1998-04-27
83 PRIOR APPLICATION NUMBER: 60/083322
84 PRIOR FILING DATE: 1998-04-28
85 PRIOR APPLICATION NUMBER: 60/083392
86 PRIOR FILING DATE: 1998-04-29
87 PRIOR APPLICATION NUMBER: 60/083495
88 PRIOR FILING DATE: 1998-04-29
89 PRIOR APPLICATION NUMBER: 60/083496
90 PRIOR FILING DATE: 1998-04-29
91 PRIOR APPLICATION NUMBER: 60/083499
92 PRIOR FILING DATE: 1998-04-29
93 PRIOR APPLICATION NUMBER: 60/083545
94 PRIOR FILING DATE: 1998-04-29
95 PRIOR APPLICATION NUMBER: 60/083554
96 PRIOR FILING DATE: 1998-04-29
97 PRIOR APPLICATION NUMBER: 60/083558
98 PRIOR FILING DATE: 1998-04-29
99 PRIOR APPLICATION NUMBER: 60/083559
100 PRIOR FILING DATE: 1998-04-29
101 PRIOR APPLICATION NUMBER: 60/083500
102 PRIOR FILING DATE: 1998-04-29
103 PRIOR APPLICATION NUMBER: 60/083742
104 PRIOR FILING DATE: 1998-04-30
105 PRIOR APPLICATION NUMBER: 60/084366
106 PRIOR FILING DATE: 1998-05-05
107 PRIOR APPLICATION NUMBER: 60/084414
108 PRIOR FILING DATE: 1998-05-06
109 PRIOR APPLICATION NUMBER: 60/084441
110 PRIOR FILING DATE: 1998-05-06
111 PRIOR APPLICATION NUMBER: 60/084637
112 PRIOR FILING DATE: 1998-05-07
113 PRIOR APPLICATION NUMBER: 60/084639
114 PRIOR FILING DATE: 1998-05-07
115 PRIOR APPLICATION NUMBER: 60/084640
116 PRIOR FILING DATE: 1998-05-07
117 PRIOR APPLICATION NUMBER: 60/084598
118 PRIOR FILING DATE: 1998-05-07
119 PRIOR APPLICATION NUMBER: 60/084600
120 PRIOR FILING DATE: 1998-05-07
121 PRIOR APPLICATION NUMBER: 60/084627
122 PRIOR FILING DATE: 1998-05-07
123 PRIOR APPLICATION NUMBER: 60/084643
124 PRIOR FILING DATE: 1998-05-07
125 PRIOR APPLICATION NUMBER: 60/085339
126 PRIOR FILING DATE: 1998-05-13
127 PRIOR APPLICATION NUMBER: 60/085338
128 PRIOR FILING DATE: 1998-05-13
129 PRIOR APPLICATION NUMBER: 60/085323
130 PRIOR FILING DATE: 1998-05-13
131 PRIOR APPLICATION NUMBER: 60/085582
132 PRIOR FILING DATE: 1998-05-15
133 PRIOR APPLICATION NUMBER: 60/085700
134 PRIOR FILING DATE: 1998-05-15
135 PRIOR APPLICATION NUMBER: 60/085689
136 PRIOR FILING DATE: 1998-05-15
137 PRIOR APPLICATION NUMBER: 60/085579
138 PRIOR FILING DATE: 1998-05-15
139 PRIOR APPLICATION NUMBER: 60/085580
140 PRIOR FILING DATE: 1998-05-15
141 PRIOR APPLICATION NUMBER: 60/085573
142 PRIOR FILING DATE: 1998-05-15
143 PRIOR APPLICATION NUMBER: 60/085704
144 PRIOR FILING DATE: 1998-05-15
145 PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 1,19e-41 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-298A-522 (1-1679)

```
QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB 134 ATGAAACACCATCCAGCAAAATGCAAAATCTATCTCTTGGGCAATCTTACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GTGTCTCTGTCTCTTCCAGAGTGCCTGCGGAGCGGAGATCCACCTTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGGACAACTGACGGTCCGGCAGGGGGAGAGCGCCACCTCAGGTGCATATTGAC 313
QY 61 AsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
DB 314 AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
DB 374 AGTGGTGGCTGGATCTCGGTGGTCTCTTGAGCAACACCCAAACGAGTACGATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAACGTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCAACCAAGACCTCTAGGTGTCACCTCTTGTGCAAGATCTCCCAAAATTTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTTCTTCAGATATCTCCATTAATGAGGGAACAAATATTAGCTCACCCTGCATAGCACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACCAAGACCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGG 673
QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
DB 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCCCGGAGCAGTCAGGGGACTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValLysValThrValAsn 220
DB 734 TGCAGTGCCTCCAATGACGTGGCGCGCGCGTGTACGGAGAGTAAGGTCAACGTGAAC 793
QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
DB 794 TATCCACCATACATTTTCAAGCAAGGAGGTACAGGTGTCCCGGTGGGCAAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
DB 854 CTGCATGTGAGCCCTCAGCAGTCCCTCAGCAGAAATCCAGTGGTACAGGATGACAA 913
QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
DB 914 AGACTGATTGAAGAAAGAGGGGTGAAGTGGAAACAGACCTTCTCTCAAAACTC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
DB 974 ATCTTCTTCAATCTCTGAACATGACTATGGAACTATACCTTGGCGTGGCCTCCAAACAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
DB 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093
```

```
QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
DB 1094 AACGGCACTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCTCTTCTTGGTCTTGACCTG 1153
QY 341 LeuLeuLysPhe 344
DB 1154 CTTCTCAAAATTT 1165
```

RESULT 24

```
US-09-978-188A-522
; Sequence 522, Application US/09978188A
; Publication No. US2003013928A1
GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC8
CURRENT APPLICATION NUMBER: US/09/978,188A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
```

; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23

; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	1.19e-41	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-978-188A-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTyrAlaIlePheThrGlyLeu 20
Db 134 ATGAACCATCCAGCAAAATGCAATCTCTTGGGCAATCTTACGGGCGTG 193
QY 21 AlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTCTCTCCAGAGAGTGCCGTCGCGAGGGAGATGCCACCTTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGGACAACGTCAGCTCCGCGAGGGGAGAGGCCACCCTCAGGTGCTATTGAC 313
QY 61 AsnArgValThrArgValAlaTyrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
Db 314 ACCGGGTACCCGGGTGGCTGGCTGAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
QY 81 LysTyrCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
Db 374 AAGTGTGCTGGATCCTCGCGTGTCTCTTGAGCAACACCCAAACGCGATACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGACGTCGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 ACCACCCAAAGACCTCTAGGTGCCACCTCATTTGTGCAAGTATCTCCCAAAATGTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTCTTCAGATATCTCCATTAATGAAGGAACAATATTAGCTCACCTGCATAGCACT 613
QY 161 GlyArgProGluProThrValThrTyrArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GTAGACCAAGGCTACGCTGCTTCTTGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
Db 674 AGTGAAGAGCATACTTGGAAATTCAGGCAATCACCAGGAGAGTCAGGGGACACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaProValValArgValArgValValThrValAsn 220
Db 734 TGCAGTGCCTCCAATCACGTCGCGCGCGCTGTGTACGGAGAGTAAAGTCAACCGTGAC 793
QY 221 TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCCACCATACATTTCAAGACCAAGGAGTACAGGTGTCCCGTGCGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAspAspLys 260
Db 854 CTGCAGTGTGAAGCCTCAGCACTCCCTCAGCAGAAATTCAGTGTGTACAGGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTCAGAGAAAGAGGGGTGAAGTGAAGAAACAGACCTTCTCTCAAAACTC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db 974 ATCTTCTCAATGCTCTGAAACATGACTATGGAACTACACTTGGTGGCTCCAAACAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGluValAlaValSerGluValSer 320
Db 1034 CTGGGCCACCAATGCCAGCATCTGCTATTGTCAGGGCGGCTCAGCGAGGTGAGC 1093
QY 321 AsnGlyThrSerArgAlaGlyCysValTyrLeuLeuProLeuLeuValLeuHisLeu 340
Db 1094 AACGGCAGCTCAGGAGGCGAGGCTGCGTCTGGCTGCTCTCTGCTTGTGCTGACCTG 1153
QY 341 LeuLeuLysPhe 344
|||||

Db 1154 CTTCTCAATTT 1165

RESULT 25

US-09-978-681A-522
; Sequence 522, Application US/09978681A
; Publication No. US20030195148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C18
; CURRENT APPLICATION NUMBER: US/09/978,681A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26

;; PRIOR APPLICATION NUMBER: 60/079664
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079689
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079663
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079728
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079786
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079920
;; PRIOR FILING DATE: 1998-03-30
;; PRIOR APPLICATION NUMBER: 60/079923
;; PRIOR FILING DATE: 1998-03-30
;; PRIOR APPLICATION NUMBER: 60/080105
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080107
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080165
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080194
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080327
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080328
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080333
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080334
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/081070
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081049
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081071
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081195
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081203
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081229
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081955
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081817
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081819
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081952
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081838
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/082568
;; PRIOR FILING DATE: 1998-04-21
;; PRIOR APPLICATION NUMBER: 60/082569
;; PRIOR FILING DATE: 1998-04-21
;; PRIOR APPLICATION NUMBER: 60/082704
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082804
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082700
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082797
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082796
;; PRIOR FILING DATE: 1998-04-23
;; PRIOR APPLICATION NUMBER: 60/083336
;; PRIOR FILING DATE: 1998-04-27
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/083392
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083495

;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083496
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083499
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083545
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083554
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083558
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083559
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083500
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083742
;; PRIOR FILING DATE: 1998-04-30
;; PRIOR APPLICATION NUMBER: 60/084366
;; PRIOR FILING DATE: 1998-05-05
;; PRIOR APPLICATION NUMBER: 60/084414
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084441
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084637
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084639
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084640
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084598
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084643
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085339
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085338
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085689
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	1.19e-41	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-978-681A-522 (1-1679)

Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrrAlaIlePheThrGlyLeu 20

Db 134 ATGAACCATCCAGCCAAATGCAATTCATTCTTGGCAATCTTCACGGGCGTG 193

	QY	21	AlaALeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
	Db	194	GCTGCTCTGTGTCTTCCAAGAGATGCCCGTCGCAGCGAGATGCCACTTCCCAAA	253
	QY	41	AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
	Db	254	GCTATGGACAAAGTGACGGTCCGGCAGGGGGAGAGGGCCACCCTCAGGTGCATTATTGAC	313
	QY	61	AsnArgValThrArgVallalaThrLeuAsnArgSerThrIleLeuTyraLaGlyAsnAsp	80
	Db	314	AACCGGGTCACCCGGGTGGCTCGCTAAAACCGCAGCACCATCTCTATGTCTGGGAATGAC	373
	QY	81	LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle	100
	Db	374	AAGTGGTGGCTGGATCCTCGCGTGGTCTCTGAGCAACACCCAAACGCAAGTAACGATC	433
	QY	101	GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp	120
	Db	434	GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC	493
	QY	121	AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu	140
	Db	494	AACCAACCAAAGACCTCTAGGGTCCACCTCATTTGTGCAGTATCTCCAAAAATGTAGAG	553
	QY	141	IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr	160
	Db	554	ATTCTCTTCAGATATCTCCATTAAATGAAGGGAACAATAATTAGCCCTCACTGCATAGCAACT	613
	QY	161	GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal	180
	Db	614	GGTAGACCAAGACCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG	673
	QY	181	SerGluAspGluTyrIleuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu	200
	Db	674	AGTGAAGACGAAATACATTGTGAAATTCAGGGCATCACCCGGCAGCAGTCCAGGGGACTACGAG	733
	QY	201	CysSerAlaSerAsnAspValAlaAlaProValValArgArgVallysValThrValAsn	220
	Db	734	TGCAGTGGCTCCAAATGACGTGGCGCGCCCGTGGTACGGAGAGTAAAGTCAACGGTAAC	793
	QY	221	TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr	240
	Db	794	TATCCACCACATACATTTTCAGAAAGCAAGGGTACAGGTGTCCCGCTGGGCACAAAAGGGGACA	853
	QY	241	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys	260
	Db	854	CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAAATCCAGTGGTACAAGGATGACAAA	913
	QY	261	ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgPropheLeuSerLysLeu	280
	Db	914	AGACTATTGAAGGAAGAAAGGGGTGAAAGTGGAAAAACAGACTTTTCCTCTCAAAATC	973
	QY	281	IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaIaSerAsnLys	300
	Db	974	ATCTTTCTTCAATGTCTTGAAATGACTATGGGAATCTACATTGCTGGGGCTCCAACAG	1033
	QY	301	LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer	320
	Db	1034	CTGGGCGCACCAATGCCAGCATCATCTATTGGTCCAGCGCGCGTCCAGCGGTGAGC	1093
	QY	321	AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValIleHisLeu	340
	Db	1094	AACGGCAGTCGAGAGGGCAGGCTGGCTGTGGTGTCTTCTTCTTGGTCTTGCACCTG	1153
	QY	341	LeuLeuLysPhe	344
	Db	1154	CTTCTCAAAATTT	1165

RESULT 26

US-09-978-194A-522

US-09-978-194A-522
; Sequence 522, Application US/09978194A

; Publication No. US20030195333A1

; FUNCTION NO: 0320
; GENERAL INFORMATION:

/ APPLICANT: Ashkenazi, Avi
 / APPLICANT: Baker Kevin P.
 / APPLICANT: Botstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Eaton, Dan
 / APPLICANT: Ferrara, Napoleon
 / APPLICANT: Filvaroff, Ellen
 / APPLICANT: Fong, Sherman
 / APPLICANT: Gao, Wei-Qiang
 / APPLICANT: Gerber, Hanspeter
 / APPLICANT: Gerritsen, Mary E.
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Grimaldi, J. Christopher
 / APPLICANT: Gurney, Austin L.
 / APPLICANT: Hillan, Kenneth J.
 / APPLICANT: Kljavin, Ivar J.
 / APPLICANT: Kuo, Sophia S.
 / APPLICANT: Napier, Mary A.
 / APPLICANT: Pan, James
 / APPLICANT: Paoni, Nicholas F.
 / APPLICANT: Roy, Margaret Ann
 / APPLICANT: Shelton, David L.
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel
 / APPLICANT: Williams, P. Mickey
 / APPLICANT: Wood, William I.
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 / TITLE OF INVENTION: Acids Encoding the Same
 / FILE REFERENCE: P2630PIC10
 / CURRENT APPLICATION NUMBER: US/09/978,194A
 / CURRENT FILING DATE: 2001-10-15
 / PRIOR APPLICATION NUMBER: 09/918585
 / PRIOR FILING DATE: 2001-07-30
 / PRIOR APPLICATION NUMBER: 60/062250
 / PRIOR FILING DATE: 1997-10-17
 / PRIOR APPLICATION NUMBER: 60/064249
 / PRIOR FILING DATE: 1997-11-03
 / PRIOR APPLICATION NUMBER: 60/065311
 / PRIOR FILING DATE: 1997-11-13
 / PRIOR APPLICATION NUMBER: 60/066364
 / PRIOR FILING DATE: 1997-11-21
 / PRIOR APPLICATION NUMBER: 60/077450
 / PRIOR FILING DATE: 1998-03-10
 / PRIOR APPLICATION NUMBER: 60/077632
 / PRIOR FILING DATE: 1998-03-11
 / PRIOR APPLICATION NUMBER: 60/077641
 / PRIOR FILING DATE: 1998-03-11
 / PRIOR APPLICATION NUMBER: 60/077649
 / PRIOR FILING DATE: 1998-03-11
 / PRIOR APPLICATION NUMBER: 60/077791
 / PRIOR FILING DATE: 1998-03-12
 / PRIOR APPLICATION NUMBER: 60/078004
 / PRIOR FILING DATE: 1998-03-13
 / PRIOR APPLICATION NUMBER: 60/078886
 / PRIOR FILING DATE: 1998-03-20
 / PRIOR APPLICATION NUMBER: 60/078936
 / PRIOR FILING DATE: 1998-03-20
 / PRIOR APPLICATION NUMBER: 60/078910
 / PRIOR FILING DATE: 1998-03-20
 / PRIOR APPLICATION NUMBER: 60/078939
 / PRIOR FILING DATE: 1998-03-20
 / PRIOR APPLICATION NUMBER: 60/079294
 / PRIOR FILING DATE: 1998-03-25
 / PRIOR APPLICATION NUMBER: 60/079656
 / PRIOR FILING DATE: 1998-03-26
 / PRIOR APPLICATION NUMBER: 60/079664
 / PRIOR FILING DATE: 1998-03-27
 / PRIOR APPLICATION NUMBER: 60/079689
 / PRIOR FILING DATE: 1998-03-27
 / PRIOR APPLICATION NUMBER: 60/079663
 / PRIOR FILING DATE: 1998-03-27
 / PRIOR APPLICATION NUMBER: 60/079728

; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	1.19e-41	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-978-194A-522 (1-1679)

Qy	1	MetLysThrIleGlnProLysMetHisnSerIleSerTrpAlaIlePheThrGlyLeu	20
Db	134	ATGAACACCATCCAGCCAAAATGCACAAATCTCTTGGGCAATCTTTCACGGGGCTG	193
Qy	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
Db	194	GCTGCTCTGTCTCTTCCAGGAGTCCCGTGGCAGCGAGATGCCACCTTCCCAAA	253
Qy	41	AlaMetAspValThrValArgGlnGlyClnuSerAlaThrLeuArgCysThrIleAsp	60
Db	254	GCTATGGACAACGTGACGTCCTCCGAGGGGAGAGCGCCCTCAGTGTCATTTGAC	313


```
QY 61 AsnArgValThrArgValAlaThrLeuAsnArgSerThrIleuTyrAlaGlyAsnAsp 80
Db 314 RACCGGACACCGGGTGGCTGGCTAAACCGCAGCACCATTCTCTATGCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
Db 374 AAGTGGTGGCTGGATCTCGCGTGGTCTCTGAGCAACACCCAAACGCGAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCGAGACAG 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCACCCAAAGACCTTAGGGTCCACCTATTGTGCAAGTATCTCCCAAAATTTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTCTCTCAGATATCTCCATTATGAAGGGAACAATATTAGCCTCACCTGCATAGCACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACCAAGAGCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
Db 674 AGTGAGACGATACTTGGAAATTCAGGGCATCCCGGAGCAGTCAAGGAGTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaLapProValValArgValLysValThrValAsn 220
Db 734 TGCAGTGGCTCCAATGACGTGGCGCGCGCGTGTGTCAGGAGAGTAAGGTCAACGTTG 793
QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCCACCATACATTTTCAAGAGCAAGGGGTACAGGTGTCCCGGTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
Db 854 CTGCAGTGTGAGGCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGAGATGACAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTCAAGAAAGAAAGGGGTGAAAGTGGAAACACAGACCTTTCTCTCMAAACTC 973
QY 281 IlePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db 974 ATCTTCTCAATGTCTCTGAACATGACTATGGAACTACACTTGGGTGGCTCCACACAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTGTTGGTCCAGGCGCTCAGCGAGGTGAGC 1093
QY 321 AsnGlyThrSerArgArgIleGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340
Db 1094 AACGGCACGTCCAGGAGGGCAGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
QY 341 LeuLeuLysPhe 344
Db 1154 CTCTCAAAATTT 1165

RESULT 27
US-09-999-829A-522
; Sequence 522, Application US/09999829A
; Publication No. US20030195344A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
```

```
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC61
; CURRENT APPLICATION NUMBER: US/09/999,829A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-999-829A-522

Alignment Scores:
Pred. No.: 1.19e-41 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-999-829A-522 (1-1679)
QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
Db 134 ATGAACCATCCAGCCAAAATGCACAAATCTATCTCTTGGGCAATCTTACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTGTCTCTTCAAGAGTGGCCGTCGCGAGGAGATGCCACCTTCCCAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGGCAACGTCACGTCGCGCAGGGGAGAGCGCCACCTCAGGTGCATATTGAC 313
QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
Db 314 AACCGGGTCACCGGGTGGCTGGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
Db 374 AAGTGGTGGCTGGATCTCGCGTGGTCTCTGAGCAACACCCAAACGCGAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCGAGACAG 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCACCCAAAGACCTTAGGGTCCACCTATTGTGCAAGTATCTCCCAAAATTTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
```

554	Db	ATTTCTTCAGATATCTCCATTAAATGAAGGGAACAATATTAGCTTCACCTGCTATAGCAACT	613
161	Qy	GlyArgProGluProThrValThrTyrArgHisileSerProLysAlaValGlyPheVal	180
614	Db	GGTAGACCAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG	673
181	Qy	SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu	200
674	Db	AGTGAAGACGGAATACTTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAAGGAGATACGAG	733
201	Qy	CysSerAlaSerAsnAspValAlaAlaProValValArgValGlyValThrValAsn	220
734	Db	TGCAGTGCCTCCAAATGACGTGGCCGCGCCGTGTACGAGAGTAAAGGTCACCGTGAAC	793
221	Qy	TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr	240
794	Db	TATCCACCATACATTTTCAGAAAGCAAGGGTACAGGTGTCCCGGTGGACAAAAGGGGACA	853
241	Qy	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAspAspLys	260
854	Db	CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGCAATTCACAGTGGTCAAGGATGACAAA	913
261	Qy	ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu	280
914	Db	AGACTGATTGAGAGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTTCCTCTCAAAACTC	973
281	Qy	IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys	300
974	Db	ATCTTCTTCATGTCTCTGAACATGACTATGGGAACCTACACTTCGCTGGCTCCCAACAAG	1033
301	Qy	LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer	320
1034	Db	CTGGGCCACACCAATGTCAGCATCATGCTATTTGGTTCAGGCGCGGTCAAGAGGTGAGC	1093
321	Qy	AsnGlyThrSerArgArgAlaGlyCysValTyrLeuLeuProLeuLeuValLeuHisLeu	340
1094	Db	AACGGCAGTCGAGAGGCGAGGCTGGGTCTGGCTGTCTGCTCTCTTCCTTCGTCCTGCACCTG	1153
341	Qy	LeuLeuLysPhe	344
1154	Db	CTTCTCAAAATT	1165

RESULT 28

US-009-978-299A-522
; Publication 522, Application US/09978299A
; Publication No. US20030199435A1
; GENERAL INFORMATION:
; APPLICANT: Aabkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey

```
/ PRIOR FILING DATE: 1998-04-08
/ PRIOR APPLICATION NUMBER: 60/081071
/ PRIOR FILING DATE: 1998-04-08
/ PRIOR APPLICATION NUMBER: 60/081195
/ PRIOR FILING DATE: 1998-04-08
/ PRIOR APPLICATION NUMBER: 60/081203
/ PRIOR FILING DATE: 1998-04-09
/ PRIOR APPLICATION NUMBER: 60/081229
/ PRIOR FILING DATE: 1998-04-09
/ PRIOR APPLICATION NUMBER: 60/081955
/ PRIOR FILING DATE: 1998-04-15
/ PRIOR APPLICATION NUMBER: 60/081917
/ PRIOR FILING DATE: 1998-04-15
/ PRIOR APPLICATION NUMBER: 60/081819
/ PRIOR FILING DATE: 1998-04-15
/ PRIOR APPLICATION NUMBER: 60/081952
/ PRIOR FILING DATE: 1998-04-15
/ PRIOR APPLICATION NUMBER: 60/081838
/ PRIOR FILING DATE: 1998-04-15
/ PRIOR APPLICATION NUMBER: 60/082568
/ PRIOR FILING DATE: 1998-04-21
/ PRIOR APPLICATION NUMBER: 60/082569
/ PRIOR FILING DATE: 1998-04-21
/ PRIOR APPLICATION NUMBER: 60/082704
/ PRIOR FILING DATE: 1998-04-22
/ PRIOR APPLICATION NUMBER: 60/082804
/ PRIOR FILING DATE: 1998-04-22
/ PRIOR APPLICATION NUMBER: 60/082700
/ PRIOR FILING DATE: 1998-04-22
/ PRIOR APPLICATION NUMBER: 60/082797
/ PRIOR FILING DATE: 1998-04-22
/ PRIOR APPLICATION NUMBER: 60/082796
/ PRIOR FILING DATE: 1998-04-23
/ PRIOR APPLICATION NUMBER: 60/083336
/ PRIOR FILING DATE: 1998-04-27
/ PRIOR APPLICATION NUMBER: 60/083322
/ PRIOR FILING DATE: 1998-04-28
/ PRIOR APPLICATION NUMBER: 60/083392
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083495
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083496
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083499
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083545
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083554
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083558
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083559
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083500
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083742
/ PRIOR FILING DATE: 1998-04-30
/ PRIOR APPLICATION NUMBER: 60/084366
/ PRIOR FILING DATE: 1998-05-05
/ PRIOR APPLICATION NUMBER: 60/084414
/ PRIOR FILING DATE: 1998-05-06
/ PRIOR APPLICATION NUMBER: 60/084441
/ PRIOR FILING DATE: 1998-05-06
/ PRIOR APPLICATION NUMBER: 60/084637
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084639
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084640
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084598
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084600
/ PRIOR FILING DATE: 1998-05-07

/ PRIOR APPLICATION NUMBER: 60/084627
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084643
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/085339
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085338
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085323
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085582
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085700
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085689
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085579
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085580
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085573
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 1.19e-41
Score: 2408.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 10
Length: 1679
Matches: 344
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-299A-522 (1-1679)
QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB 134 ATGAACACCATCCAGCCAAAATGCACAAATCTATCTCTGGCAATCTTCACGGGGGTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTCTGTCTCTTCCAAAGAGTGCCTGCGGAGGAGATGCCACCTTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGGACACAGTGCAGTCCGCGAGGGGAGAGCCGCCCTCAGTCACCTATTGAC 313
QY 61 AsnArgValThrArgValAlaAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
DB 314 AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
DB 374 AAGTGGTCCCTGGATCTCTCGCGTGGTCTTCTTGAGCAACACCCCAACGCGATACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAACGTTGATGTATGACGAGGGGCCCTTACACCTCTCGTGCACAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATGCAACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACCAAGCCCTACGGTTACTTTGAGACACATCTCTCCCAAGCGGTGGTTTGTG 673
QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
```


1 PRIOR APPLICATION NUMBER: 60/081229
1 PRIOR FILING DATE: 1998-04-09
1 PRIOR APPLICATION NUMBER: 60/081955
1 PRIOR FILING DATE: 1998-04-15
1 PRIOR APPLICATION NUMBER: 60/081817
1 PRIOR FILING DATE: 1998-04-15
1 PRIOR APPLICATION NUMBER: 60/081819
1 PRIOR FILING DATE: 1998-04-15
1 PRIOR APPLICATION NUMBER: 60/081952
1 PRIOR FILING DATE: 1998-04-15
1 PRIOR APPLICATION NUMBER: 60/081838
1 PRIOR FILING DATE: 1998-04-15
1 PRIOR APPLICATION NUMBER: 60/082568
1 PRIOR FILING DATE: 1998-04-21
1 PRIOR APPLICATION NUMBER: 60/082569
1 PRIOR FILING DATE: 1998-04-21
1 PRIOR APPLICATION NUMBER: 60/082704
1 PRIOR FILING DATE: 1998-04-22
1 PRIOR APPLICATION NUMBER: 60/082804
1 PRIOR FILING DATE: 1998-04-22
1 PRIOR APPLICATION NUMBER: 60/082700
1 PRIOR FILING DATE: 1998-04-22
1 PRIOR APPLICATION NUMBER: 60/082797
1 PRIOR FILING DATE: 1998-04-22
1 PRIOR APPLICATION NUMBER: 60/082796
1 PRIOR FILING DATE: 1998-04-23
1 PRIOR APPLICATION NUMBER: 60/083336
1 PRIOR FILING DATE: 1998-04-27
1 PRIOR APPLICATION NUMBER: 60/083322
1 PRIOR FILING DATE: 1998-04-28
1 PRIOR APPLICATION NUMBER: 60/083392
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083495
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083496
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083499
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083545
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083554
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083558
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083559
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083500
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083742
1 PRIOR FILING DATE: 1998-04-30
1 PRIOR APPLICATION NUMBER: 60/084366
1 PRIOR FILING DATE: 1998-05-05
1 PRIOR APPLICATION NUMBER: 60/084414
1 PRIOR FILING DATE: 1998-05-06
1 PRIOR APPLICATION NUMBER: 60/084441
1 PRIOR FILING DATE: 1998-05-06
1 PRIOR APPLICATION NUMBER: 60/084637
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084639
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084640
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084598
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084600
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084627
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084643
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/085339
1 PRIOR FILING DATE: 1998-05-13
1 PRIOR APPLICATION NUMBER: 60/085338

1 PRIOR FILING DATE: 1998-05-13
1 PRIOR APPLICATION NUMBER: 60/085323
1 PRIOR FILING DATE: 1998-05-13
1 PRIOR APPLICATION NUMBER: 60/085582
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085700
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085689
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085579
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085580
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085573
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085704
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 1-19e-41 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-544A-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB 134 ATGAAACCATCCAGCCAAATAATGCACAATCTATCTCTTGGGCAATCTTCACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTCTGTCTCTTCCAAGAGTGCCTGCGAGCGAGATGCCACCTTCCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGGACACGTGACCGGTCCGGCAGGGGAGAGCGGCCACCTCAGGTGCATATTGAC 313
QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
DB 314 AACCGGGTCACCGGGTGGCTGCTAAACCGCAGCACCATCTCTATGTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuSerAsnThrGlnThrGlnTyrSerIle 100
DB 374 AAGTGTGCTGGATCCTCGCGTGGTCTCTTGAGCAACACCCAAACGAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTCAAGTATCTCCCAAAATTTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTCTTTCAGATATCTCCATTAAAGAGGAACAATATTAGCCTCACTCTGCATGCAACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACCAGACCTACGGTTACTTTGGAGACACATCTCTCCCAAGCGGTGGTTGGTTGTG 673
QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
DB 674 AGTGAAGACGAATATCTTGAATTCAGGGCATCACCGGGAGCAGTCAGGGGACTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
DB 734 TGCAGTGCCTCCAATGACGTGGCGGCCCGCTGTGTAGCGAGAGTAAAGGTACCGGTGAAC 793

Qy	221	TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr	240
Db	794	TATCCACATACATTTCAGAGGCCAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA	853
Qy	241	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAspAspLys	260
Db	854	CTGCAAGTGAAGCCTCAGCAGTCCCTCAGCAGAATTCCAGTGGTCAAGGATGACAAA	913
Qy	261	ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu	280
Db	914	AGACTGATTGAAGCAAGAAAGGGGTGAAGTGGAAAACAGACCTTTCCTCTCAAAACTC	973
Qy	281	IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys	300
Db	974	ATCTTCTTCATGTCTCTGAACATGACTATGGGAACCTACACTTCGTGGCTCCCAACAG	1033
Qy	301	LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer	320
Db	1034	CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCAGGCGCGCTCAGCAGGTGAGC	1093
Qy	321	AsnGlyThrSerArgArgAlaGlyCysValTyrLeuLeuProLeuLeuValLeuHisLeu	340
Db	1094	AACGGCAGCTCAGAGGGCAGGCTGGGTCTGGCTGTCTCTTCCTTCGCTTCGACCTG	1153
Qy	341	LeuLeuLysPhe	344
Db	1154	CTTCTCAAAATT	1165

RESULT 30

US-09-978-665A-522

Sequence 522, Application US/09978665A

Publication No. US20030199437A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J

APPLICANT: Kljavin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2630PIC19

CURRENT APPLICATION NUMBER: US/09/978,665A

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: 09/918595

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

1 PRIOR FILING DATE: 1998-04-15
1 PRIOR APPLICATION NUMBER: 60/081952
1 PRIOR FILING DATE: 1998-04-15
1 PRIOR APPLICATION NUMBER: 60/081838
1 PRIOR FILING DATE: 1998-04-15
1 PRIOR APPLICATION NUMBER: 60/082568
1 PRIOR FILING DATE: 1998-04-21
1 PRIOR APPLICATION NUMBER: 60/082569
1 PRIOR FILING DATE: 1998-04-21
1 PRIOR APPLICATION NUMBER: 60/082704
1 PRIOR FILING DATE: 1998-04-22
1 PRIOR APPLICATION NUMBER: 60/082804
1 PRIOR FILING DATE: 1998-04-22
1 PRIOR APPLICATION NUMBER: 60/082700
1 PRIOR FILING DATE: 1998-04-22
1 PRIOR APPLICATION NUMBER: 60/082797
1 PRIOR FILING DATE: 1998-04-22
1 PRIOR APPLICATION NUMBER: 60/082796
1 PRIOR FILING DATE: 1998-04-23
1 PRIOR APPLICATION NUMBER: 60/083336
1 PRIOR FILING DATE: 1998-04-27
1 PRIOR APPLICATION NUMBER: 60/083322
1 PRIOR FILING DATE: 1998-04-28
1 PRIOR APPLICATION NUMBER: 60/083392
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083495
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083496
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083499
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083545
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083554
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083558
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083559
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083500
1 PRIOR FILING DATE: 1998-04-29
1 PRIOR APPLICATION NUMBER: 60/083742
1 PRIOR FILING DATE: 1998-04-30
1 PRIOR APPLICATION NUMBER: 60/084366
1 PRIOR FILING DATE: 1998-05-05
1 PRIOR APPLICATION NUMBER: 60/084414
1 PRIOR FILING DATE: 1998-05-06
1 PRIOR APPLICATION NUMBER: 60/084441
1 PRIOR FILING DATE: 1998-05-06
1 PRIOR APPLICATION NUMBER: 60/084637
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084639
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084640
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084598
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084600
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084627
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/084643
1 PRIOR FILING DATE: 1998-05-07
1 PRIOR APPLICATION NUMBER: 60/085339
1 PRIOR FILING DATE: 1998-05-13
1 PRIOR APPLICATION NUMBER: 60/085338
1 PRIOR FILING DATE: 1998-05-13
1 PRIOR APPLICATION NUMBER: 60/085323
1 PRIOR FILING DATE: 1998-05-13
1 PRIOR APPLICATION NUMBER: 60/085582
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085700
1 PRIOR FILING DATE: 1998-05-15

1 PRIOR APPLICATION NUMBER: 60/085689
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085579
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085580
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085573
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085704
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 1-19e-41 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-665A-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMethHisAsnSerIleSerTTPAlaIlePheThrGlyLeu 20
DB 134 ATGAAACCATCCAGCCAAAATGCACAATCTATCTCTTGGCAATCTTACCGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTCTGTGTCCTTCCAGGAGTGCCCGTGCAGCGGAGATGCCACCTTCCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGGACACAGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGTGCACATATTGAC 313
QY 61 AsnArgValThrArgValAlaTTPLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp 80
DB 314 AACCGGGTCACCGGGTGGCTGCTAAACCGCAGCAGCATCTCTATGTGGGAATGAC 373
QY 81 LysTyrCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
DB 374 AAGTGGTGCCTGGATCCTCGCGTGTCTTCTTGACCAACACCCAAACGCGATCAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAACGTGGATGTGTATCGCAGGGGCCCTTACACCTGCTCGGTGCAGACAG 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCAACCCAAAGACCTCTAGGGTCCACCTCATTTGTCAAGTATCTCCCAAAATTTGAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTTCTTCAGATATTCCTCAATTAATGAAGGAACAATATTAGCCTTACCTGCATAGCACT 613
QY 161 GlyArgProGluProThrValThrTTPArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACCAAGACCTTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTG 673
QY 181 SerGluAspGluTyrIleuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
DB 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGCGAGCAGTCAGGGGACTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
DB 734 TGCAGTGCCTCCANTGACGTGGCCCGCGCTGTGTACGGAGAGTAAGGTACACCTGAGAC 793
QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyIleGlnLysGlyThr 240
DB 794 TATCCACCACATCATTTCCAGAACCCAAAGGTCACAGGTGTCCCGTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrIlyAspAspLys 260
DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGGTACAAGGATGACAAA 913


```
QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTTCTCTCAAAACTC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
974 ATCTTCTTCATGTCTCTGACATGACTATGGGAACTACACTTGGCTGGCTCCACACAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGTCAGCGAGGTGAGC 1093
QY 321 AsnGlyThrSerArgArgAlaGlyCysValTyrLeuLeuProLeuValLeuHisLeu 340
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
1094 AACGGCACGTCGAGAGGGCAGGCTGCGTCTGGCTGCTGCTCTTCTGTGGTCTTGACCTG 1153
QY 341 LeuLeuLysPhe 344
Db |||||||||||
1154 CTTCTCAAAATTT 1165
```

Search completed: May 28, 2004, 15:28:57
Job time : 624 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 28, 2004, 12:59:14 ; Search time 3099 Seconds
(without alignments)
3314.808 Million cell updates/sec

Title: US-10-017-084A-523
Perfect score: 2408
Sequence: 1 MKTIQPMKNSISWAIFTGL.....RRAGCVMLPLLVHLLKRF 344

Scoring table: BLOSUM30
Xgapop 1.0 , Xgapext 0.1
Ygapop 1.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US10017084/runat_28052004.125907.29900/app.query.fasta_1.519
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum30 -TRANS=human40.cdi -LIST=100
-DOALIGN=200 -THR SCORE=ptc -THR MAX=100 -THR MIN=0 -ALIGN=30 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10017084 @CNG 1 1 3437 @runat_28052004.125907.29900 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.1 -XGAPOP=6
-FGAPEXT=7 -XGAPOP=1 -YGAPEXT=0.1 -DELOP=6 -DELEX=7

Database :

EST:**

- 1: em estba:**
- 2: em esthum:**
- 3: em estin:**
- 4: em estnu:**
- 5: em estov:**
- 6: em estpl:**
- 7: em estro:**
- 8: em htc:**
- 9: gb est1:**
- 10: gb est2:**
- 11: gb htc:**
- 12: gb est3:**
- 13: gb est4:**
- 14: gb est5:**
- 15: em estfun:**
- 16: em estom:**
- 17: em gss hum:**
- 18: em gss inv:**
- 19: em gss pin:**
- 20: em gss vrt:**
- 21: em gss fun:**
- 22: em gss man:**
- 23: em gss mus:**
- 24: em gss pro:**
- 25: em gss rod:**
- 26: em gss phg:**
- 27: em gss vrl:**
- 28: gb gss1:**

29: gb_gss2:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2369	98.4	1808	11	AK045973	Mus muscu
2	2369	98.4	1808	11	AK046377	Mus muscu
3	2023	84.0	874	29	AY406347	Homo sapi
4	1996	82.9	874	29	AY406349	Homo sapi
5	1863	77.4	1039	10	BE798585	Mus muscu
6	1798	74.7	3166	11	AK042854	Mus muscu
7	1784	74.1	773	29	AY406348	Pan trogl
8	1736	72.1	856	13	BUI55617	AGENCOURT
9	1720	71.4	765	14	CD354474	UI-M-GMO-
10	1714	71.2	11493	29	AY404090	Mus muscu
11	1696	70.5	2798	11	AK028345	Mus muscu
12	1693	70.3	11490	29	AY404088	Homo sapi
13	1691	70.3	8928	11	AK090134	Mus muscu
14	1688	70.1	12485	29	AY404418	Homo sapi
15	1684	69.9	14278	11	AY318958	Rattus no
16	1684	69.9	14278	11	AY321317	Rattus no
17	1683	69.9	8259	11	BC038478	Mus muscu
18	1682	69.9	12304	29	AY404420	Mus muscu
19	1679	69.7	14278	11	AY318958	Rattus no
20	1679	69.7	14278	11	AY321317	Rattus no
21	1676	69.6	10481	11	AK090138	Mus muscu
22	1675	69.6	10481	11	AK090138	Mus muscu
23	1672	69.5	9744	29	AY405009	Homo sapi
24	1671	69.4	8315	11	AK090135	Mus muscu
25	1670	69.4	22715	28	AQ839851	69115-C79
26	1667	69.3	14771	28	AQ839854	260113-C5
27	1665	69.2	10560	28	AQ839853	260113-C5
28	1665	69.2	12485	29	AY404419	Pan trogl
29	1665	69.2	9567	29	AY405011	Mus muscu
30	1662	69.0	11490	29	AY404089	Pan trogl
31	1661	69.0	8928	11	AK090134	Mus muscu
32	1661	69.0	11493	29	AY404090	Mus muscu
33	1660	68.9	7866	29	AY417659	Mus muscu
34	1660	68.9	15970	28	AQ839852	260113-C5
35	1660	68.9	10638	28	AQ839855	69115-C78
36	1659	68.9	8329	11	AK090130	Mus muscu
37	1659	68.9	12349	11	AK090125	Mus muscu
38	1659	68.9	22715	28	AQ839851	69115-C79
39	1659	68.9	12349	11	AK090125	Mus muscu
40	1657	68.8	14771	28	AQ839854	260113-C5
41	1654	68.7	9097	29	AY400949	Mus muscu
42	1651	68.6	8329	11	AK090130	Mus muscu
43	1651	68.6	6468	29	AY400046	Mus muscu
44	1650	68.5	6972	29	AY405714	Homo sapi
45	1649	68.5	6468	29	AY400044	Homo sapi
46	1648	68.5	9184	29	AY402246	Homo sapi
47	1647	68.4	7518	11	BC058249	Mus muscu
48	1647	68.4	8936	11	AK090121	Mus muscu
49	1647	68.4	11415	29	AY418622	Mus muscu
50	1646	68.4	6836	29	AY405716	Mus muscu
51	1646	68.4	15970	28	AQ839852	260113-C5
52	1645	68.3	8315	11	AK090135	Mus muscu
53	1645	68.3	9022	29	AY402248	Mus muscu
54	1644	68.3	8373	11	BC051010	Mus muscu
55	1643	68.2	8259	11	BC038478	Mus muscu
56	1643	68.2	8936	11	AK090121	Mus muscu
57	1642	68.2	11490	29	AY404088	Homo sapi
58	1639	68.1	9330	11	AK090118	Mus muscu
59	1638	68.1	8532	29	AY417357	Homo sapi
60	1638	68.0	10655	11	AK090136	Mus muscu
61	1638	68.0	10638	28	AQ839855	69115-C78
62	1638	68.0	10655	11	AK090136	Mus muscu

C	63	1637.4	68.0	9097	29	AY400949	Mus muscu
	64	1637.2	68.0	9022	29	AY402248	Mus muscu
C	65	1636.4	68.0	8160	29	AY416949	Homo sapi
	66	1636.2	67.9	7596	11	AY383707	Rattus no
C	67	1635.1	67.9	10560	28	AQ839853	260113-C5
	68	1634.5	67.9	9184	29	AY402246	Homo sapi
C	69	1632.6	67.8	8044	11	AK090132	Mus muscu
	70	1631.4	67.7	2768	11	AK030681	Mus muscu
C	71	1630.9	67.7	7134	11	AY325252	Rattus no
	72	1630.9	67.7	11487	29	AY418620	Homo sapi
C	73	1630.7	67.7	6840	11	BC038794	Mus muscu
	74	1630.7	67.7	6852	11	AK090117	Mus muscu
C	75	1630.3	67.7	6885	11	AF549895	Xenopus l
	76	1629.5	67.7	12304	29	AY404420	Mus muscu
C	77	1628.9	67.6	9183	29	AY400947	Homo sapi
	78	1628.6	67.6	7964	29	AY416951	Mus muscu
C	79	1628.2	67.6	7884	29	AY417657	Homo sapi
	80	1628	67.6	7694	11	AK030315	Mus muscu
C	81	1627.9	67.6	9567	29	AY405011	Mus muscu
	82	1627.6	67.6	979	12	BG261691	BC058249
C	83	1627.2	67.6	7518	11	BC058249	Mus muscu
	84	1626.8	67.6	9744	29	AY405009	Homo sapi
C	85	1626.8	67.6	11415	29	AY418622	Mus muscu
	86	1624.2	67.5	7884	29	AY417657	Homo sapi
C	87	1623.1	67.4	7232	11	AF034176	AF034176
	88	1623	67.4	9664	28	BH771023	LLMGtag74
C	89	1622.4	67.4	8175	11	AK090120	Mus muscu
	90	1622.1	67.4	7060	11	BC043838	Xenopus l
C	91	1621.9	67.4	8293	11	AK090126	Mus muscu
	92	1620.9	67.3	7763	11	BC047348	Mus muscu
C	93	1620.8	67.3	6921	28	AF101618	AF101618
	94	1620.2	67.3	9835	11	AK090131	Mus muscu
	95	1619.8	67.3	7232	11	AF034176	AF034176
	96	1619.3	67.2	6966	11	AY383712	Rattus no
C	97	1618.9	67.2	11490	29	AY404089	Fan trogl
	98	1618.2	67.2	8268	11	AK090127	Mus muscu
	99	1617.9	67.2	8284	11	AK090128	Mus muscu
	100	1617.8	67.2	7694	11	AK030315	Mus muscu

ALIGNMENTS

RESULT 1
 LOCUS AK045973
 DEFINITION Mus musculus adult male corpora quadrigenima cDNA, RIKEN full-length enriched library, clone:B230328N06 product:NEUOTRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.
 ACCESSION AK045973
 VERSION AK045973.1 GI:26337738
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
 2
 20493374
 11042159
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multipillar sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861
 4

THE RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

5
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

6 (bases 1 to 1808)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Takagi, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://phantom.gsc.riken.go.jp/.

FEATURES

source

1. 1808
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="FANTOM DB:B230328N06"
 /db_xref="MGI:2411356"
 /db_xref="taxon:10090"
 /clone="B230328N06"
 /sex="male"
 /tissue_type="corpora quadrigenima"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="adult"
 204. 1238
 /note="unnamed protein product; NEUOTRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus] (SWISSPROT|Q62718, evidence: FASTA, 99.4%ID, 92.1%length, match=951) putative"
 /codon_start=1
 /protein_id="BAC32555.1"
 /db_xref="GI:26337739"

CDS

204. 1238
 /note="unnamed protein product; NEUOTRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus] (SWISSPROT|Q62718, evidence: FASTA, 99.4%ID, 92.1%length, match=951) putative"
 /codon_start=1
 /protein_id="BAC32555.1"
 /db_xref="GI:26337739"
 /translation="MKTQAKMNSISWAIPTGLAALCLFGQVIVRSGDPTFPKAMDN VTRVGSGATLRCTIDNTRVAMLRSTILYAGNDKWLQDFRVVLLNTQYISIEI QNVDYDEGPTVCSQTDHPKTSRVHLIVQSPKIVETSSDISINEGNSILSTCIAT

GRPEPTVWRHISPKAVGFVSEDEYLEIQGITREQSGEYECASNDVAAPVVRVKVT
VNPYPYISAKGTGVPVQKGTLOCEASAVPSAEFWFKODKRLVEGKGKVKVNRPF
LSKLTFFNVSDHGYNTCTVASNKLGHINASIMLFGPAVSEVNNGTSRRAGCIIWLP
LLVHLHLKLF"

ORIGIN

Alignment Scores:

Pred. No.: 1.77e-29 Length: 1808
Score: 2369.00 Matches: 337
Percent Similarity: 99.13% Conservative: 4
Best Local Similarity: 97.97% Mismatches: 3
Query Match: 98.38% Indels: 0
DB: 11 Gaps: 0

US-10-017-084A-523 (1-344) x AK045973 (1-1808)

Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerThrAlaIlePheThrGlyLeu 20
Db 204 ATGAACCATCCAGCGGCAAAATGACAAATCTATCTCGTGGGCAATCTTCACGGGGCTG 263
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 264 CGGGCTCTGCTCTTCCAGAGAGTGCCTGCGGTAGCGGAGATGCCACCTTTCCCAA 323
Qy 41 AlaMetAspAenValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 324 GCTATGGACACAGTGCAGTGCAGCGGCGGAGAGCGCCACCTCAGGTGCACAAATTGAC 383
Qy 61 AsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
Db 384 AACCGAGTCAACCGGTGGCTGGCTAAACCGCAGTACCATCTCTATGCTGGAAATGAC 443
Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAenThrGlnThrGlnTyrSerIle 100
Db 444 AAGTGTGCTAGATCCTCGTGTGCTCTCTGAGTAACCCAGACCCAGATCAGCAT 503
Qy 101 GluIleGlnAenValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 504 GAGATCCAGAGATGGAGTGTAGCATGAGGCGCTTATATACCTGCTCGGTACAGACAGAC 563
Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 564 AACCACTAGACTCCAGGCTCCACTCATTTGTAAGTATCTCCAAATTTGTAGAG 623
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAenIleSerLeuThrCysIleAlaThr 160
Db 624 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAACATCAGCCCTCACTTCATAGCCACA 683
Qy 161 GlyArgProGluProThrValThrTyrArgHisIleSerProLysAlaValGlyPheVal 180
Db 684 GGTAGACCGAGAGCTCAGTAACCTGGAGACATATTTCTCCAAAGGCGTTGGCTTTGTG 743
Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
Db 744 AGTGAGATGAGTACTTGGAGATCCAGGCATCACTCGGACACAGTACGGGAGTACGAG 803
Qy 201 CysSerAlaSerAenAspValAlaAProValValArgArgValLysValThrValAsn 220
Db 804 TGCAGCGCTCCACGACGTCGGCGCCACCTGCTGACGAGAGTGAAGTCCACCGTGAAC 863
Qy 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlnLysGlyThr 240
Db 864 TATCCACATACATCTCAGAACTTAAGGACAGGTGTCCCGGTGGGCGAGAGGGAGCT 923
Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAspLys 260
Db 924 CTGCAGTGTGAAGCTTCGCGAGTCCCTTCAGCAGATTTCAATGCTTCAGGATGACAAA 983
Qy 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAenArgProPheLeuSerLysLeu 280
Db 984 AGACTGTGCGAAGGAAGAGAGGAGTCAAGTGGAAACAGACCTTTCTTCAAAACTC 1043
Qy 281 IlePhePheAenValSerGluHisAspTyrClyAsnTyrThrCysValAlaSerAsnLys 300

Db 1044 ACCTTTTCAACGCTCTGACATGACTATGGNACTACACATGTGTGGCTCCCAACAG 1103
Qy 301 LeuGlyHisThrAenAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1104 CTGGTCCACACCAACGCCAGCATCATATTTGGTCCCGTGTCTGTCAGTGAGGTCAAC 1163
Qy 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
Db 1164 ATGGGACATCAAGGAGGAGGAGGCTGCATTTGGCTCTCCCTCTTCTGGTCTTACACCTG 1223
Qy 341 LeuLeuLysPhe 344
Db 1224 CTCCTCAAAATTT 1235

RESULT 2

AK046377

LOCUS

DEFINITION

AK046377

1808 bp mRNA linear

Mus musculus adult male corpora quadrigemina cDNA, RIKEN

full-length enriched library, clone:B230377K17 product:NEUROTRIMIN

PRECUSOR (GP65) homolog [Rattus norvegicus], full insert sequence.

AK046377

HTC; CAP trapper.

Mus musculus

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

1808 bp mRNA linear

Mus musculus adult male corpora quadrigemina cDNA, RIKEN

full-length enriched library, clone:B230377K17 product:NEUROTRIMIN

PRECUSOR (GP65) homolog [Rattus norvegicus], full insert sequence.

AK046377

HTC; CAP trapper.

Mus musculus

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Oheato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, I., Sogabe, I., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES

source

```
1..1808
    /organism="Mus musculus"
    /mol_type="mRNA"
    /strain="C57BL/6J"
    /db_xref="PANTOM:DB:B230377K17"
    /db_xref="MGI:2411773"
    /db_xref="taxon:10090"
    /clone="B230377K17"
    /sex="male"
    /tissue type="corpora quadrigemina"
    /clone_lib="RIKEN full-length enriched mouse cDNA library"
    /dev_stage="adult"
204..1238
    /note="unnamed protein product; NEUROTRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus] (SWISSPROT|062718, evidence: FASTV, 99.4%ID, 92.1%length, match=951) putative"
    /codon_start=1
    /protein_id="BAC32695.1"
    /db_xref="GI:26338019"
    /translation="MTKIQAKWHSISWAIPTGLAALCLFGQVPRSGDATFFPKAMDN VTRQGSATLURCIDNRTVAVLNRSITLYAGNDKWLDPVLLSNTQYSIEI QNVDVDSPTVCSQVDNHPKTSKVLIVQSPKIVEISSDISINGNNISLTQSIAT GRPEPTVWHISPKAVGFVSEVLEIQITRQSGEYECASNDVAAVPRPVKVT VNYPPYISEAKGTGVPVQKGLQCEASNPASFPQFQDKDLVVEGKGVKVENRPF LSKLTFNVSHEDIGNVTCVASNKLGHINASIMLFGPAVSEVNNGTSRRAGCIWLPL LVLHLHLKLF"
```

CDS

```
1..77e-29 Length: 1808
2369..0 Matches: 337
Percent Similarity: 99.33% Conservative: 4
Best Local Similarity: 97.97% Mismatches: 3
Query Match: 98.38% Indels: 0
DB: 11 Gaps: 0
```

ORIGIN

```
Alignment Scores:
Pred. No.: 1..77e-29 Length: 1808
Score: 2369..0 Matches: 337
Percent Similarity: 99.33% Conservative: 4
Best Local Similarity: 97.97% Mismatches: 3
Query Match: 98.38% Indels: 0
DB: 11 Gaps: 0
```

US-10-017-084a-523 (1-344) x AK046377 (1-1808)

```
Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTIPAlaIlePheThrGlyLeu 20
Db 204 ATGAAACCATCCAGGCAAAATGCACAAATCTATCTCGTGGCAATCTTCAAGGGGCTG 263
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProlys 40
Db 264 GCGGCTCTGTGCTCTTCCAGAGAGTGGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 323
Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuAtgCysThrIleAsp 60
Db 324 GCTATGGACACGTGACCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 383
```

```
Qy 61 AsnArgValThrArgValAlaAlaTIPLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
Db 384 AACCGAGTCAACCCGGTGGCGTGGCTAAACCGAGTACCATCTCTATGTGGAAATGAC 443
Qy 81 LysTyrCysLeuAepProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
Db 444 AAGTGGTGGCTAGATCTCTGTGGTCTCTCTGAGTAAACCCAGACCCAGTACAGATT 503
Qy 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 504 GAGATCCAGAAATGGATGTGTACGATGAGGGCCCTTATACCTGCTCGGTACAGACAGAC 563
Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 564 AACCACTTAAAGCCTCCAGGCTCCACCTATTGTACAAGTATCTCCCAAAATTTGTAGAG 623
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 624 ATTTCTTCAGATATCTCCANTTAAGAGGAGNACAAATCAGCTCCTTTCATAGGCCACA 683
Qy 161 GlyArgProGluProThrValThrTIPArgHisIleSerProLysAlaValGlyPheVal 180
Db 684 GGTAGACGGAGCCTCAGTAAACCTGGAGACATATTTCTCCCAAGGCGCTTGGCTTTGTG 743
Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
Db 744 AGTAGAGATGATGATCTTGGAGATCCAGGGCATCTCGGAAACAGTCAAGGAGTACGAG 803
Qy 201 CysSerAlaSerAsnAepValAlaAProValValArgArgValLysValThrValAsn 220
Db 804 TGACAGCGCTCCACAGCAGTGGCGGCACCAAGTGTGTAAGAGTGAAGTCAAGTCAAC 863
Qy 221 TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 864 TATCACCATACATCTCAGAGCTAAGGACAGTGTCCCGTGGGCGGAGAGGAGT 923
Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnThrTyrLysAspAspLys 260
Db 924 CTGAGTGTGAGCTTCCGAGTCCCTTCAGAGAAATTCATGTTCAAGAGTACGAAA 983
Qy 261 ArgLeuIleGluGlyLysGlyValLysValLysValLysValLysValLysValLysLeu 280
Db 984 AGACTGTGCAAGAAAGAGGAGTCAAAGTGAAACAGACCTTTCTTCAAAACTC 1043
Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db 1044 ACCTTTTCAACGCTCTGAACATGACTATGGGAACATACACATGTGTGGCTCCAAAG 1103
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1104 CTGGGTCAACCAACGCGCAGCATCATGTTATTTGGTCCCGTGTCTGTCTGAGTCAAC 1163
Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTIPLeuLeuProLeuLeuValLeuHisLeu 340
Db 1164 AATGGGACATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1223
Qy 341 LeuLeuLysPhe 344
Db 1224 CTCTCAAAATTT 1235
```

```
RESULT 3
AY406347
LOCUS
DEFINITION Homo sapiens HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
AY406347 genomic survey sequence.
ACCSSION AY406347.1 GI:39762321
VERSION AY406347.1
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```

REFERENCE
AUTHORS
1 (bases 1 to 874)
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
AUTHORS
2 (bases 1 to 874)
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
location/Qualifiers
1..874
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>874
/locus_tag="HCM2527"
gene
ORIGIN
US-10-017-084A-523 (1-344) x AY406347 (1-874)
Alignment Scores:
Pred. No.: 2,57e-24 Length: 874
Score: 2023.80 Matches: 288
Percent Similarity: 99.31% Conservative: 0
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 84.04% Indels: 2
DB: 29 Gaps: 1
57 CysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyr 76
Db 2 TGCACATATTGACACACCGGCTCCCGGGTGGCTGCTTAACCGCAGCACCATCTCTAT 61
Qy 77 AlaGlyAsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThr 96
Db 62 GCTGGATGACAGTGTGTGGATCTCTGGTGGTCTCTGAGCAACCCCAACG 121
Qy 97 GlnTyrSerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSer 116
Db 122 CAGTACAGCATCGAGATCCAGACGTGGATCTGTATGACGAGGGCCCTTACACCTGCTCG 181
Qy 117 ValGlnThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerPro 136
Db 182 GTGCAGACAGACACACCCACCAAGACCTCTAGGGTCCACCTCATTTGTCAAGTATCTCCC 241
Qy 137 LysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThr 156
Db 242 AATTTGTAGATTTCTTCAGATATCTCCATTAATGAGGGAACAATATTAGCTCACC 301
Qy 157 CysIleAlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLys--- 175
Db 302 TGCATAGCAACTGGTAGACACGAGCTACGGTTACTTGGAGACACATCTCTCCCAACCC 361
Qy 176 ---AlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGlu 194
Db 362 GCACGGTGTGGCTTGTGAGTGAAGAGCAATCTTGGAAATTCAGGGCATCACCCGGGAG 421
Qy 195 GlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArg 214
Db 422 CAGTCAGGGGACTACGAGTGCAGTGCCTCCCAATGACGTGGCCGCCCGTGGTACGGAGA 481
Qy 215 VallysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValPro 234
Db 482 GTAAAGGTACCGTGAACTATCCACCATACATTTTCAGAGGCCAAGGGTACAGGTGTCTCCC 541

```

```

QY 235 ValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGln 254
Db 542 GTGGGACAAAAGGGGACACTGCTGAGTGTGAAGCTTCAGAGTCCCCCTCAGCAGAAATTCAG 601
QY 255 TrpTyrIysAspAspLysArgLeuIleGluGlyLysGlyValLysValGluAsnArg 274
Db 602 TGGTACAGGATGACAAAGACTGATTGAAGAAAGAAAGGGTGAAGTGGAAACAGA 661
QY 275 ProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThr 294
Db 662 CTTTCTCTCTCAAACTCATCTTCTCAATCTCTCTGAACATGACTATGGGAACATACACT 721
QY 295 CysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGly 314
Db 722 TGGTGGCTTCCACACAGCTGGGCGACACCAATGCCAGCATCATGCTATTGGTCCAGGC 781
QY 315 AlaValSerGluValSerAsnGlyThrSerArgAlaGlyCysValTrpLeuLeuPro 334
Db 792 GCCGTGACGAGGTGAGCAACGGCAGCTCGAGGAGGCGAGGCTGGCTGCTGCTGCT 841
QY 335 LeuLeuValLeuHisLeuLeuLysPhe 344
Db 842 CTTCTGGTCTTGCACCTGCTTCTCAAAATT 871
RESULT 4
AY406349
LOCUS
AY406349
DEFINITION
Mus musculus HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
ACCESSION
AY406349
VERSION
AY406349.1 GI:39762323
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 874)
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
AUTHORS
2 (bases 1 to 874)
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
location/Qualifiers
1..874
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>874
/locus_tag="HCM2527"
gene
ORIGIN
Alignment Scores:
Pred. No.: 8,46e-24 Length: 874
Score: 1996.80 Matches: 282
Percent Similarity: 98.62% Conservative: 4
Best Local Similarity: 97.24% Mismatches: 2
Query Match: 82.92% Indels: 2
DB: 29 Gaps: 1

```

US-10-017-084A-523 (1-344) x AY406349 (1-874)

```

QY 57 CysThrLeuAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyr 76
Db 2 TGCACAAATTGACACCGAGTACCCGGGTGGCTTAAACCCGAGTACCATCTCTAT 61
QY 77 AlaGlyAenAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThr 96
Db 62 GCTGGAAATGACAAAGTGGTGGCTAGATCTCTGGTGGTCTCTCTGAGTACACCCAGACC 121
QY 97 GlnTyrSerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSer 116
Db 122 CAGTACAGCAATGAGATCCAGAAATGTGATGTGACGATGAGGGCCCTTATACCTGCTCG 181
QY 117 ValGlnThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerPro 136
Db 182 GTACAGACAGACACACCCCTAGACCTCCAGGGTCCACCTCATGTACAGTATCTCCC 241
QY 137 LysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThr 156
Db 242 AAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAACATCAGCTCACT 301
QY 157 CysIleAlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLys--- 175
Db 302 TGCATAGCCACAGGTAGACCGGAGCCTACAGTAACCTGGAGACATATTTCTCCAAAGCCC 361
QY 176 ---AlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGlu 194
Db 362 GCAGCGGTGGCTTTGTGAGTGAGATGAGTACTCTGGAGTCCAGGGCACTCCGGAA 421
QY 195 GlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProValValArg 214
Db 422 CAGTCAGCGAGTACGAGTGCAGCGCTCCCAACGACGTGGCGGCACCACTGGTACGAAGA 481
QY 215 ValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValPro 234
Db 482 GTGAAGTGCACCGTGAATATCTCCACCATACATCTCAGAAGCTAAGGGCACAGGTGTCCTCC 541
QY 235 ValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGln 254
Db 542 GTGGGGCAGAAAGGGGACTCTCAGTGTGAAGCTTCGACAGTCCCTTCAGCAGAAATTTCAA 601
QY 255 TrpTyrLysAspAspLysArgLeuIleGluGlyLysGlyValLysValGluAsnArg 274
Db 602 TGGTTCAAGGATGACAAAGAACTGGTCGAAGAAAGAGGAGTCAAAGTGGAAACAGA 661
QY 275 ProPheLeuSerLysLeuIlePheAsnValSerGluHisAspTyrGlyAsnTyrThr 294
Db 662 CTTTCTCTTCAAACTCACCTTTTCAACGTCTCTGACATGATATGGGAACATACACA 721
QY 295 CysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGly 314
Db 722 TGTGTGGCTCCAAAGCTGGGTACACCAACGCCAGCATCATGCTATTGGTCCCGGT 781
QY 315 AlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuPro 334
Db 782 CTTGTAGTGGTCAACATGGGACATCAAGGAGGCGAGGCTGATTTGGCTCTCTCCCT 841
QY 335 LeuLeuValLeuHisLeuLeuLysPhe 344
Db 842 CTTCTGGTCTTACACCTGCTCTCAAAATT 871

```

```

RESULT 5
BE798585
LOCUS BE798585 1039 bp mRNA linear EST 20-SEP-2000
DEFINITION 601581610F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935955 5',
mRNA sequence.
ACCESSION BE798585
VERSION BE798585.1 GI:10219783
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 1039)
NIH-MGC http://imgc.ncbi.nlm.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L10M779 row: d column: 04
High quality sequence stop: 849.
Location/Qualifiers
1..1039

FEATURES

source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3935955"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Alignment Scores:
Pred. No.: 6.57e-21 Length: 1039
Score: 1863.90 Matches: 263
Percent Similarity: 72.54% Conservative: 17
Best Local Similarity: 68.13% Mismatches: 13
Query Match: 77.40% Indels: 94
DB: 10 Gaps: 38

US-10-017-084A-523 (1-344) x BE798585 (1-1039)

QY 5 GlnProLysMethHisAsnSerIleSerTrpAlaIlePheThrGlyLeuAlaLeuCys 24
Db 4 CGAGGAGG-----AAC-----GGTTGG---ATC-----GCACACTGT 33
QY 25 LeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsn 44
Db 34 CTG---CAT---CAATTA-----TTGCC---TCA---GATCT- 59
QY 45 ValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThr 64
Db 60 ---TCA-----GGC-----AGGTGCACCTATTGCACACCGGGTCGCC 92
QY 65 ArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeu 84
Db 93 CGAGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGATGACAGTGGTGGCTG 152
QY 85 AspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsn 104
Db 153 GATCTCTGGGTGGTCTCTCTGAGCAACACCCAAACGACGATCAGATCCAGAAC 212
QY 105 ValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLys 124
Db 213 GTGATGTGTATGACGAGGGCCCTTACACTGCTCGTGCAGACAGCAACCAACCCAAAG 272
QY 125 ThrSerArgValHisLeuIleValGlnValSerProLysIleValGluIleSerSerAsp 144
Db 273 ACCTTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGATTCTTCAGAT 332

Qy 145 ILeSerIleAenGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGlu 164
 Db 333 ATCTCCATTAAAGGGAACAATATTAGCTCCTACCTGATAGCAACTGGTAGACCAGAG 392
 Qy 165 ProThrValThrTrrAtcGHisIleSerProIysAlaValGlyPheValSerGluAspGlu 184
 Db 393 CCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTTGGCTTTGTGAGTGAAGCGAA 452
 Qy 185 TyrLeuGluIleGlnGlyThrArgGluGlnSerGlyAspTyrGluCysSerAlaSer 204
 Db 453 TACTTGGAAATTCAGGGCATCACCAGGAGCAGTCAAGGGGACTACGATGAGTGCCTCC 512
 Qy 205 AsnAspValAlaAlaProValValArgValIysValThrValAsnTyrProProTyr 224
 Db 513 AATACGCTGGCGCGCCGCTGACGAGAGTAAAGGTCACCGTGAATCTCCACCATAC 572
 Qy 225 IleSerGluAlaIleGlyThrGlyValProValGlyGlnIysGlyThrLeuGlnCysGlu 244
 Db 573 ATTTCAGAACCAAGGGTACAGGTGTCTCCCGTGGGACAAAGGGGACACTCGAGTGTGA 632
 Qy 245 AlaSerAlaValProSerAlaGluPheGlnTrrTyrIysAspAspIysAsnIleGlu 264
 Db 633 GCCTCAGCAGTCCCTCAGCAGATTCAGTGTGTACAGGATGACAAAGACTGATTGAA 692
 Qy 265 Gly---LysIysGlyValLys---ValGluAsnArgProPheLeuSer-----LysLeu 280
 Db 693 GGAACAGACAGGGGT---GAACAGTTGGAAACACAGACCTTTT---TCTCTCTCAAAAGTC 746
 Qy 281 Ile---PhePheAsnVal-----SerGluHisAspTyr-GlyAsnTyrThrCysValAl 297
 Db 747 ATTCTCTTTTCAATGCTCTCGANCC---ATGACTATGGGAACACTACACTTGGCGGGC 803
 Qy 297 a-SerAsnLysLeuGlyHisThrAsnAla---Ser-----I 308
 Db 804 TCCCA---AAAGCTGGGCACACCAATGCCAGATCATGCTATTGCGTAATAGAGCAGC 860
 Qy 308 le---MetLeuPheGlyProGlyAlaValSerGluValSer---Asn---Gly----- 322
 Db 861 TAGAAAAGTTGGTA---CCA-----GTG---GAG---AGCCACAATGCCGATAGGACA 905
 Qy 323 -----Thr-----SerArg----- 325
 Db 906 GTCCAGTCTACAGCCCGCTGTGAGCGAGCCAAAGAGCAGCGGGCGCGAGTGAGCAA 965
 Qy 326 -----ArgAlaGly---CysValTrpLeuLeuProLeuLeuValLeuHisLeuLeuL 343
 Db 966 GCTAGAGCGCGGTTGGTGGCTCTGG---TGCCCG-----GTC-----A 1001
 Qy 343 YS-----Phe 344
 Db 1002 ATTGTGGCGGCTTC 1015

RESULT 6
 AK042854
 LOCUS
 DEFINITION Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730031E08 product:NEUROTRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.
 ACCESSION AK042854
 VERSION AK042854.1 GI:26089310
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 HIGH-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 93279253
 PUBMED 10349636
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itch, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, F., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 4

The RIKEN Genome Exploration Research Group Phase II Team and the
 PANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 5

The PANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 6

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Koya, S., Kurihara, C., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Nakamura, M., Nishi, K., Nomura, K., Miyazaki, A., Murata, M.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 Direct Submission

JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 7

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)

JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 8

cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.

JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 9

Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/.

JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 10

Location/Qualifiers
 1. .3166
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="FANTOM_DB:A730031E08"
 /db_xref="MGI:2407957"
 /db_xref="taxon:10090"
 /clone="A730031E08"
 /tissue type="cerebellum"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="7 days neonate"

JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 11

misc_feature
 1. .3166
 /note="NEUROTRIMIN PRECURSOR (GP65) homolog [Rattus

norvegicus] (SWISSPROT|Q62718, evidence: FASTY, 99.4%ID,
92.1*length, match=951)"

ORIGIN

Alignment Scores:
Pred. No.: 1,94e-17 Length: 3166
Score: 1798.80 Matches: 261
Percent Similarity: 31.83% Conservative: 49
Best Local Similarity: 26.80% Mismatches: 17
Query Match: 74.70% Indels: 647
DB: 11 Gaps: 118

US-10-017-084A-523 (1-344) x AK042854 (1-3166)

```
QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB 206 ATGAACACCATCCAGGCAAAATGACAAATCTATCTCGTGGCCAACTTTCACGGGGCTG 265

QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 266 GCGGCTCTGTGCTCTCTCCAAAGAGTGCGGTGCGTAGCGGAGATGCCACCTTCCCAA 325

QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 326 GCTATGGACACGTCAGCGTCAAGGCGGGGAGAGCGCCACCTCAGGTGCACAAATTGAC 385

QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
DB 386 AACCGAGTCACCCGGGTGGCTGGCTAAACCGCAGTACCATCTCTATGCTGGAAATGAC 445

QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrSerIle 100
DB 446 AAGTGTGCTAGATGCTCGTGTGCTCTCTGAGTAAACCCAGACCCAGTACAGCAT 505

QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB 506 GAGATCCAGATGTGGATGTGATGATGAGGCGCCCTTATACCTGCTCGTACACAGAC 565

QY 121 AsnHisProLysThrSerArgValHisLeuIleValGln-----ValSer--- 135
DB 566 AACCAACCTTAAGACCTCCAGGGTCCACCTCATTTGTACAAGTGGGTGGGCTGGCTGG 625

QY 136 ---ProLys-----Ile-----Val 139
DB 626 AGGCTGAGTGGGTGGGGAATATACAACTACTGATTTTTCACAACTCTAATC 685

QY 140 Glu-----Ile-----SerSer-----Asp 144
DB 686 CAAGCTAGTGGGTGGTCTCCCGCAGCAAGTCTCTCTGGTGGTCACTTTGAAGCTAGAC 745

QY 145 IleSer-----IleAsn-----GluGlyAsn----- 151
DB 746 ---ACGGAAGCTTTCATCAATTTACTTTTGTAGTTGAACCAAGTTTTCCTCTATTCAG 802

QY 152 -----Asn----- 152
DB 803 ATTATGTTTGTACAAATATTGCTCAATTTATTTGTTCCCTGGCTTTTCCTCTCTTA 862

QY 153 -----IleSerLeu---ThrCys---IleAlaThrGlyArg----- 162
DB 863 GCATTTTAAATATGTTTCATACAACTACAAGTTGTTTATTT---TTA---AGACAAGAA 916

QY 163 -----Pro----- 163
DB 917 TTTTAATGTTCTTCGGTGTGTATATATATATGTTTCCCTGGCTTTTCCTCTCTTA 976

QY 164 ---GluPro-----ThrVal----- 168
DB 977 ACAAAGCCAGAACAGTACCCAGATCTTATCCCAACCAATCCCTCCACACACCCCAATTA 1036

QY 169 -----Trp-----ArgHis----- 171
DB 1037 TAAGTATAGGGTGCTGTCTCTCTCTCCATCCAACTCCAGTTTGGCTTCCCACTGCTCT 1096
```

```
QY 172 ---Ile-----Ser-----ProLys----- 175
DB 1097 GCTATAAGACTGGATTCAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1156

QY 176 -----Ala---ValGlyPheVal----- 180
DB 1157 GGCTTAATGTTTGTGGGTCCTCCCGTGTGTTTGTGGGCTTTGTGGCAATTTCTCCAG 1216

QY 181 -----SerGluAspGluTyrLeuGluIle---Gln---GlyIle----- 191
DB 1217 GTTCTCATCTCT---CTGCTTCTCATATCACAGGTCTGTGTGTGTGTGTGTGTGTGT 1267

QY 192 -----ThrArgGluGln----- 196
DB 1268 AAAATCAGATGGTCTCGAGGAGCAGCA---CAACATTTTAAACAAGTAGATGAATTTCTAG 1324

QY 196 r-----GlyAspTyr---GluCys---Ser-----AlaSer 204
DB 1325 TTACTGAACAACAGCTTTGGGC---TACATGTCTGTGTTTCTGACGAGAGAAAGGCTC 1381

QY 204 rAsnAspValAlaAla-Pro-----ValValArg-----Arg--- 214
DB 1382 AAAT---ATTACTGACCCCTGGGGCTTTTCTTTCGCAAAATAGGGTAAATGTGAGGAGTG 1438

QY 215 ---ValLysValThr---Val---AsnTyr-----Pro----- 222
DB 1439 GGGTGAAGATTTACATTTATATGTAGGTAAACTAAGCCCTTAGGAGAAAGCCCTCACCTGT 1498

QY 223 -----ProTyr----- 224
DB 1499 GGAGGACTATTACCTGTTGTGTCATCATGTATGATGTCCTCTTGAATTTCTTTTCAA 1558

QY 225 -----Ile-----SerGluAlaLys---GlyThr- 231
DB 1559 ATACAGTGAATATTTTAAACATTTAGTCATGTTTATAGT---AAATTAATAACTT 1612

QY 232 -----GlyValPro-----ValGlyGlnLys--- 238
DB 1613 GCITTTGTTCTCTGAGAACTAAACATACCATGAAGTAAATTTCTGTGGA---TTTTTTG 1669

QY 239 ---Gly-----ThrLeu----- 241
DB 1670 TGGGTTTCTCCTGCTCCTGCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1729

QY 242 ---Gln-----Cys-----Glu-----AlaSer-----AlaValProS 250
DB 1730 TCAGCATGATGTCAGGTGTCAGGAGAGCCATGAAGTTGCTCTTGTGCAACAGCTGCTT 1789

QY 250 exAlaGluPheGlnTrp---Tyr---Lys---Asp----- 258
DB 1790 CC-----TGAAGTACACTTGAGAGTAGGATGAAACCTGAGTGTGAGTGTGAGTGTGAGA 1837

QY 259 ---AspLys-----Arg---Leu-----Ile----- 263
DB 1838 GAGACAAAAGAAATAGGGGATTCGAGAAGACAAATTCGAAGAGTGTGAGGAGGAGCCTGTG 1897

QY 264 -----Glu----- 265
DB 1898 AGCAGAGAGGAAAGCAGAAATGCCATCATGAAACCAACAGAGCTACGAGGAGTGAATGG 1957

QY 265 ly-----LysLysGly----- 268
DB 1958 GGCAAGCAGCCTAGATGAGATGAGACTATGTTAGAAATGAGGGGACACTTGAGCATATGTAGA 2017

QY 269 -----ValLysVal-----GluAsnArg-----Pro- 275
DB 2018 GGGAGGTGAAGGTAGCAGCTGACTGCAATGATGACGGCTGTGGTAGAGTATGGTCACTTC 2077

QY 276 -----PheLeuSer-----LysLeu----- 280
DB 2078 AGGGTTTATCACTTTTGTCTGCTGCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2137
```

```

QY 281 -----Ile-----PhePhe-----283
Db 2138 CTTTATTGATCTATAAATAGTACTTTTTTTTTCGAAACAGGTTAGTGCATAATAGAG 2197
QY 284 -----Asn-----ValSer-----286
Db 2198 TTTTAAATAGATTCATAGCAGTACTTGTGAGTGCTTTATATAATAGCAGATAGGTACT 2257
QY 287 -----Glu-----His-----288
Db 2258 GCTATGTGAAATTTTGTGTGTATACATTTTCAACGTACAAAAAGCTTTTCCTTGTA 2317
QY 289 -----Asp-----Tyr-----290
Db 2318 GATAGAAATAGACAAAATAAAGTTAAGGTCACAGTCTGTGGGGTAGCTTGTGGAA 2377
QY 291 -----GlyAsn-----Tyr-----Thr-----294
Db 2378 TGTCTCGGGGAAGCCATCTGCCATCTCTATTAGGCGAGTACCTCACAGTCTTGTGG 2437
QY 295 -----Cys-----ValAlaSer-----Asn-----LysLeuGly-----302
Db 2438 CAGAATGTCCTCAATGACCAAGATGGCTAGGAGATTGGAGCAGACAGCTTTCGTCAGGA 2497
QY 303 -----His-----Thr-----Asn-----Ala-----306
Db 2498 AGCAGCACCACACTATGAACTGAAAGAGGACAAAATAGAAAAAAGAGAGCACCCTTAGAA 2557
QY 307 -----Ser-----I 308
Db 2558 AATAAAGAACAGTTTGTAGTCAATGTTTGTGTATACATCTTCTTGGACACATCGTATA 2617
QY 308 Le-----Met-----Leu-----PheGly-----312
Db 2618 TACGTGCTATAATAGTAGACTGACTTTTACACATGGGAAATTAATAAATGCTTATTGA 2677
QY 313 -----ProGlyAlaVal-----SerGlu-----318
Db 2678 AGCAATGCTTGGAAATTATAGTACAAAGATCTTACATGGGCTCTGAGAGAAAAGGATGG 2737
QY 319 Val-----Ser-----AsnGlyThrSerArgAlaGly-----Cys 329
Db 2738 ATAGCTGGAGTGTGGGGGGC-----AGCAGGAGGAGGAGGAGGACACAGCCTACATCTGT 2794
QY 330 Val-----Tip-----331
Db 2795 CTTCACCTCACGTCGAAGTAATAGAAATGTCTAATCCATAGCCAGGTGTTTACGTCTGT 2854
QY 332 -----Leu-----LeuPro-----Leu-----338
Db 2855 GACTTGGCTAGGTGCCCTCTTCCCATGACACACCATCTTGTAGTATTGGAATCTCATCTTG 2914
QY 338 -----338
Db 2915 GGCTAATTTTGAATGCTGATGGGTGATTGATCTGGAAACAGCTGGTTAAAAAAGGC 2974
QY 339 -----His-----Leu-----Leu-----341
Db 2975 ATTGGCTTGTACACAGACTCAGCCCAAGCTAATCCGCTGTCAATATGCTCGCGCTGAGG 3034
QY 342 -----LeuLys-----Phe 344
Db 3035 ATTATTGACAGTTAATGAATAGAGGACCATAGTTT 3070

RESULT 7
AY406348
LOCUS
DEFINITION
Pan troglodytes HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY406348
VERSION
AY406348.1 GI:39762322
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)

```

```

ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1 (bases 1 to 773)
AUTHORS
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 773)
AUTHORS
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
location/Qualifiers
1..773
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<!.>773
/locus_tag="HCM2527"
gene
ORIGIN
Alignment Scores:
Pred. No.: 5.52e-20 Length: 773
Score: 1784.80 Matches: 253
Percent Similarity: 98.44% Conservative: 0
Best Local Similarity: 98.44% Mismatches: 2
Query Match: 74.12% Indels: 2
DB: 29 Gaps: 1
US-10-017-084A-523 (1-344) x AY406348 (1-773)
QY 57 CysThrIleAspAsnArgValThrArgValAlaTirPleuAsnArgSerThrIleLeuTyr 76
Db 2 TGCACTATTGACAAACCGGGTCAACCCGGGTGGCTTAAACCCGACGACCATCTCTAT 61
QY 77 AlaGlyAsnAspLysTyrCysLeuAspProArgValValLeuLeuSerAsnThrGlnThr 96
Db 62 GCTGGGAATGACAGTGGTGGTGGATCCTCGGTGGTCTTCTGAGCAACACCCAAACG 121
QY 97 GlnTyrSerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSer 116
Db 122 CAGTACAGCATTCAGATCCAGAACGGTGTGTATGACGAGGCGCTTACCTGCTGCG 181
QY 117 ValGlnThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerPro 136
Db 182 GTGCAGACAGACAAACCAACCAAGAGCCTCTAGGGTCCACTCATTTGTCNNNTATCTCCC 241
QY 137 LysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThr 156
Db 242 AAAATTTGTAGAGATTTCTTCAGATATCTCCATTAACAGAGGAACAATATCAGCCTCAC 301
QY 157 CysIleAlaThrGlyArgProGluProThrValThrTirPArgHisIleSerProLys--- 175
Db 302 TGCAATAGCAACTGTGTAGACCAAGAGCCTACGGTTACTTGGAGACACATCTCCCCAAACC 361
QY 176 ---AlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGlu 194
Db 362 GCAGCGGTTGGCTTTGTGAGTAGAGCAATATCTTGGAAATTCAGGGCATCACCGGGAG 421
QY 195 GlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArg 214
Db 422 CAGTCAGGGGACTACAGAGTGCATGCTCCAATGACGTGGCGCGCGCGCTGGGTACGAGA 481

```

```

QY 215 VallysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValPro 234
Db 482 GTAAAGGTCAACCGTGACTATCCACATACATTTCAGAACCAAGGTACAGGTGTCCTCC 541
QY 235 ValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGln 254
Db 542 GTGGGACAAAAGGGGACACTGCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATCCAG 601
QY 255 TrpTyrIleAspAspLysArgLeuIleGluGlyLysGlyValLysValGluAsnArg 274
Db 602 TGGTACAGGATGACAAAAGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAACAGAGA 661
QY 275 ProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThr 294
Db 662 CCTTTCCTCCAAACTCATCTCTCAATGTCTCTGACATGACTATGGGAACACTACACT 721
QY 295 CysValAlaSerAnLysLeuGlyHisThrAsnAlaSerIleMetLeuPhe 311
Db 722 TGGGTGGCCCTCCAAAGAGCTGGGGCCACACCAATGCCAGCATCATGTATTT 772

RESULT 8
BU155617 856 bp mRNA linear EST 03-SEP-2002
LOCUS AGENCOURT_7973225 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6166839
5', mRNA sequence.
ACCESSION BU155617
VERSION BU155617.1 GI:22669149
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NTH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCFTD/DTF
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M13527 row: m column: 16
High quality sequence stop: 593.

FEATURES
source
1..856
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6166839"
/tissue_types="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_72"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN
Alignment Scores:
Pred. NO.: 7.56e-19 Length: 856
Score: 1736.10 Matches: 251
Percent Similarity: 74.57% Conservative: 10
Best Local Similarity: 71.71% Mismatches: 7
Query Match: 72.10% Indels: 83
DB: 13 Gaps: 16

US-10-017-084A-523 (1-344) x BU155617 (1-856)

QY 2 Lys-----ThrIle---Gln-----ProLysMetHisAsnSerIleSerTrpAla 15

```

```

Db 12 GAATGGGGTCTGTGGGTACCTTCTCTGCTCCCT-----GGAAGTGCCTCGTGGTCG 62
QY 16 IlePheThrGlyLeuAlaAlaLeuCysLeuPhe-----GlnGlyValProValArg 32
Db 63 TGTCCTCTCAGGC-----TGCTG-TTCTTGTACCCACAGAGTGCCTGCGC 109
QY 33 SerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGlyLeuSer 52
Db 110 AGCGGAGATGCCACCTTCCCAAAAGCTATGGCAACGTCGCGTCCGGAGGGGAGAGC 169
QY 53 AlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArgSer 72
Db 170 GCCACCTCAGGTGCACACTATTGACACCCGGGTACCCGGGTGGCCCTGGCTAAACCCGAGC 229
QY 73 ThrIleLeuTyrAlaGlyAsnAspLysTyrCysLeuAspProArgValValLeuLeuSer 92
Db 230 ACCATCTCTATGCTGGGAATGACAAGTGGTGGCTCGCTCGCTGCTCTCTCTGAGC 289
QY 93 AsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGluGlyPro 112
Db 290 AACRCCCAACCGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATCAGCAGGGCCCT 349
QY 113 TyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeuIleVal 132
Db 350 TACACCTGCTCGGTGCAGACAGACACACCCACCAAGACCTCTAGGGTCCACCTCATTTGTG 409
QY 133 GlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsn 152
Db 410 CAAGTATCTCCCAAAATTTAGAGATTCTTCAGATATCTCCATTATGAAGGGAACAAT 469
QY 153 IleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHisIle 172
Db 470 ATTAGCTCACCTGCATAGCACTGTGTAGACAGACCTACGGTTACTTGGAGACATC 529
QY 173 SerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIleThr 192
Db 530 TCTCCCAAGCGGTTCGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGCCTCACC 589
QY 193 ArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProValVal 212
Db 590 CGGGAGCATCAGGGGACTACGAGTGCAGTGCCTCCCAATGACGTGGCGCGCGCTGGTA 649
QY 213 ArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThrGly 232
Db 650 CGGAGAGTAAGGTCACTCCCTGAACTATCCACATACATTTCCAGAACCCAGGGTACAGT 709
QY 233 Val-ProValGlyGlnLysGlyThrLeuGln-CysGluAlaSerAlaValProSerAlaG 252
Db 710 GTCCCCCGTGGGACAAAAGGGGACACTGCAGTGTGTGAAAACCTCAGCAGTCCCTCAGCAG 769
QY 252 Lu-PheGlnTyrIleLysAsp-----AspLysArgLeuIleGluGlyLysLys 267
Db 770 AATTCAGTGTGGTACAGGGATGAACCAAGACTGAT-----TTG---AAGGGAAAAAAA 820
QY 268 GlyValLysValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGlu 287
Db 821 GGG-----GTGGAA---AGG----- 832
QY 288 HisAspTyrGlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSer 307
Db 833 -----GGG-----AAA-----AACGAA----- 844
QY 308 IleMetLeuPheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAla 327
Db 845 -----CCT----- 847
QY 328 GlyCysValTrpLeuLeuProLeu 335
Db 848 -----TTCCCTCTC 856

RESULT 9
CD354474

```

LOCUS CD354474 765 bp mRNA linear EST 15-JUL-2003
 DEFINITION UI-M-GMO-cgd-g-16-0-UI.r1 NIH BMAP GMO Mus musculus cDNA clone
 IMAGE:30361215 5', mRNA sequence.
 ACCESSION CD354474
 VERSION CD354474.1 GI:31146975
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC <http://mgi.nci.nih.gov/>
 1 (bases 1 to 765)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pYX-5.
 Location/Qualifiers
 1..765
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30361215"
 /tissue_type="whole brain"
 /dev_stage="1, 5 and 15 days newborn"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH BMAP GMO"
 /note="Organ: Brain; Vector: pYX-Asc; Site 1: Ecor I;
 Site 2: Not I; The library was constructed according
 to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was size
 selected according to mRNA size fraction. Ligated with Ecor
 I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is CGAAGTGAAT. This library was created for the University
 of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

ORIGIN
 Alignment Scores:
 Pred. No.: 9.17e-19 Length: 765
 Score: 1720.00 Matches: 247
 Percent Similarity: 88.03% Conservative: 3
 Best Local Similarity: 86.97% Mismatches: 3
 Query Match: 71.43% Indels: 31
 DB: 14 Gaps: 3

US-10-017-084A-523 (1-344) x CD354474 (1-765)

Qy 7 LysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeuAlaLeuCysLeuPhe 26
 Db 5 AAATGACAAATTCATCTCGTGGGCAATTCACGGGGCTGGCGGCTCTGCTCTTC 64
 Qy 27 GlnGlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThr 46
 Db 65 CAAGAGTGGCGGTGGTGGAGATGCCACCTTCCCAAGCTATGAGCAACGTCACG 124
 Qy 47 ValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgVal 66

Db 125 GTCAGGCAGGGGAGAGCGCCACCTCAGGTGCACAAATTGACAAACCGAGTCACCGGGTG 184
 Qy 67 AlaTrpLeuAsnArgSerThrIleLeuTyrrAlaGlyAsnAspLysTrpCysLeuAspPro 86
 Db 185 GCCTGGCTAAACCCGAGTACCATCTCTATGCTGGAATGACAAAGTGGTGGCTAGATCCT 244
 Qy 87 ArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAsp 106
 Db 245 CGTGTGGTCTCTCTGAGTAAACCCAGACCCAGTACAGCATTTGAGATCCAGATGTCGAT 304
 Qy 107 ValTyrAspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSer 126
 Db 305 GTGTACCATGATGGGCGCCCTTATACCTGCTCGGTACAGACAGACCAACCCCTTAAGACCTCC 364
 Qy 127 ArgValHisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSer 146
 Db 365 AGGTCCACCTCATGTACAGTATCTCCCAAAATTTAGAGATTTCTTCAGATATCTCC 424
 Qy 147 IleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThr 166
 Db 425 ATTAATGAAGGGAACAACATCAGCTCCTCATGTCATAGCCACAGGTAGACCGGAGCTACA 484
 Qy 157 ValThrTrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyrIleu 186
 Db 435 GTAACCTGGAGACATATTTCTCCCAAGCGCTTGGCTTTGTAGTGAGGATGAGTACCTG 544
 Qy 137 GluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAsp 206
 Db 545 GAGATCCAGGGCATCACTCGGGAACAGTCAGGCGAGTACGAGTGCAGGCGCTCCACGAC 604
 Qy 237 ValAlaIleProValValArgArgValLysValThrValAsnTyrProTyrIleSer 226
 Db 605 GTGGCGGCACCACTGGTGTACGAGAGTCAAGGTCAACCGTCAACTATCCACCATCATCTCA 664
 Qy 227 GluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSer 246
 Db 665 GAACCTAAGGCACANGTGTCCCGTGGGGCAGAAAGGGGACTCTGCAGTGTGAAGCTTCG 724
 Qy 247 -AlaValProSerAlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGly 266
 Db 725 CAGT---CCTTCAGCAAGATTTTCATGCT---CNGATGACAAA----- 761
 Qy 266 sLysGlyValLysValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSe 286
 Db 761 ----- 761
 Qy 286 rGluHisAsp 289
 Db 762 -----GAC 764

RESULT 10
 AY404090
 LOCUS Mus musculus SACS gene, VIRTUAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AY404090
 VERSION AY404090.1 GI:39760073
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 11493)
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 11493)
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.

TITLE

JOURNAL
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA

COMMENT
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

FEATURES

source

Location/Qualifiers

1..11493

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

<1..>11493

/gene="SACS"

/locus_tag="HMC1774"

ORIGIN

Alignment Scores:

Pred. No.: 3.02e-13 Length: 11493
 Score: 1714.20 Matches: 303
 Percent Similarity: 10.67% Conservative: 30
 Best Local Similarity: 9.71% Mismatches: 8
 Query Match: 71.19% Indels: 2779
 DB: 29 Gaps: 243

US-10-017-084A-523 (1-344) x AY404090 (1-11493)

```

QY      1 MetLysThr-----Ile----- 4
Db      2032 ATGAAAACCTGCAATGGCTAAAGTTCGCGCTTAGTACAAGACTGATCAATCCTGAA 2091
QY      5 -----Gln-----Pro-----Lys----- 7
Db      2092 AACATGGGGTTGAGCAGTCAGGGCAAGAGAGAGCTCTTACTGTAGGATTAAATATT 2151
QY      7 ----- 7
Db      2152 TTGGAAGAATACCTTCGCTGCAGATATTTTAAAGAGCTACTTCAAAATGCTGATGAT 2211
QY      8 -----Met----- 8
Db      2212 GCAATGCCACAGATGCAAGCTTCATGATGATGATGAGAGGAATATGGACATACGGGAA 2271
QY      9 -----His----- 9
Db      2272 AATCTCTGACCCAGGATGGCAGCTGTGTCATGGACCTGCTCTGTGGTCATTCAACAAT 2331
QY      9 ----- 9
Db      2332 TCTGAATTCAGATTCAGATTTCTTAAACATAACGAGGTTAGGAGAGTCTTTAAAAAGG 2391
QY      10 -----AsnSer----- 11
Db      2392 GGAGAAGTTGACAAGTTGGGAATTTGGTCTTGGTTTAAATCTGTGTACCATCACT 2451
QY      11 ----- 11
Db      2452 GACATTCCTCATATTATGACGAGAGAAATTATGATAATGTTTATGATCAAAACATAAATCAT 2511
QY      12 IleSer-----TrpAla----- 15
Db      2512 ATCAGCAACACATTAAAGATAGATCGAATCTCGGAATCAAAATTAATTGGAGTAAGCAG 2571
QY      16 -----Ile-----Phe----- 17
Db      2572 CAGAAAAGATTAGGAAGTTCCCAACACAGTTCAAAACATTATATGATGATTTGGCTGT 2631
QY      18 -----ThrGly-----Leu----- 20
Db      2632 CAGTTACCTTTGGCTGTGTAAGCTCCTTACAGCTACAATGGAACCTCTTTCCGACTGTCC 2691
QY      21 -----Ala-----Ala 22

```

```

Db      2692 TTTAGAACACAGCAGGAGCAAAAGTAGTGAAGTTAGCAGTACTTGTCTACAATACTGCG 2751
QY      23 -----LeuCys-----Leu-----Phe----- 26
Db      2752 GATATTACTCCCTAGTGGATGAATTTAGTCTTTGTGGGCACAGACTTATCAATTTTACT 2811
QY      27 GlnGlyVal----- 29
Db      2812 CAGAGTGTAAACTCGATGATTTGAAATACTTGAAATTTGAGAAACCAATCCTAGCTTA 2871
QY      30 -----Pro 30
Db      2872 GCACAAGATACATCATATTAAGAAAAAAGTTTGGCCCTCCAAAGCAITGAATGCACCA 2931
QY      31 Val----- 31
Db      2932 GTTTAAAGTGTTTTAAAGAGAGCTGCTAAACTCATGAAGACTTTGTAGCAGCAGCAACAG 2991
QY      31 ----- 31
Db      2992 AAGCTTCCACGGATGTGCCAAAGTCATCTTGCAATCTTCAGATCACAGTCGAAGAATTC 3051
QY      32 -----Arg-----Ser-----Gly----- 34
Db      3052 CACCATGTGTTTAGGAGGATTCGTGACTTACAGTCACCACTATTTCGAGGTCCAGATGAT 3111
QY      35 Asp-----AlaThr-----Phe----- 38
Db      3112 GACCCAGCTACTCTCTTTGAAATGGCTAAATCTGGCCAACTCAAAAAGCCATCAGATGAG 3171
QY      39 -----Pro-----LysAla-----MetAsp----- 43
Db      3172 TTGCCCAAAAGACAGCTAGATTTGATACCATGGCTTATATGACATGCATGGATACAGGA 3231
QY      44 -----Asn----- 44
Db      3232 GAAGCTCTCAAGTTTTCCTTGAATGAAGTGAAGAGATTAGGGCTGTTCTTGTGGG 3291
QY      45 -----Val-----ThrVal----- 47
Db      3292 GCAGTAGGGTTCTCTTGCATGAAACCCAGAGAACAGAGTGGACCGTGAACACACATA 3351
QY      47 ----- 47
Db      3352 GGAGAGTGTGTTGCTATTATTACCTCTACGAATCAAAAAGGGTTGCCAATTCACATCAAT 3411
QY      47 ----- 47
Db      3412 GGGTGCTTTGCTGTACTTCAATAGGAAGAAATCTGGAAGACAGATACAAAAGTCCA 3471
QY      48 -----Arg-----Gln----- 49
Db      3472 TGGATACCAATTCATGAGGCATGTCTGTTGAAAGCTTACTTACAAGCCCTCAGTGTGC 3531
QY      50 -----GlyGlu----- 51
Db      3532 TTACGGGACCTAGCCATTTGGTGTGAGCTGACTGATTATATTACTATGTCAGTGTGGCT 3591
QY      52 -----Ser----- 52
Db      3592 GATCTGTATCTAGTTTCATGATGACTTCTCTGTGATCTGTAAAGGATTTTATGAAGACATT 3651
QY      53 Ala-----Thr----- 54
Db      3652 GCTCATGGAAGGGGAGGAGTTGACCAAGTCTTCTGTGATGGGTCTATGTGGTTTCC 3711
QY      55 -----Leu-----Arg----- 56
Db      3712 ATGAAGATGTGAGGTTTCTGATGACTCTATATTCAAAAGGAAGATGTTGGTTTCAGA 3771
QY      56 ----- 56

```


QY 124 -----Lys---Thr-----Ser-----126
Db TCTATTTGTGAATAGATAAGCCACAGAGGCTCTGAATGTCCTATTCACTAAAGGC 6051
QY 127 -----Arg-----ValHis-----129
Db 6052 AAGATCACTGATGGAGCCGATTGAAGAGGAAGCAATTCACGGCTCTGTAAATTGACAGT 6111
QY 130 -----Leu-----Ile---ValGln-----133
Db 6112 GTTACTAAAGAGACAGCTCAAGGACATACAGTTCAACAAATACCTACACTATGGAT 6171
QY 133 -----133
Db 6172 ACTGAGGATTCGAAGGAATCTGACACATGGCTCATCTGTATAGATCAGGATTTTCA 6231
QY 134 -----ValSer-----135
Db 6232 AGTATGMAAAGTATCCAGAGTGTAAATACAGCTCACAGAACCAAGATATCACCCCTT 6291
QY 136 ---Pro-----Lys-----137
Db 6292 TTCCACGCTGGTAGTAGCAGCTGCATTACTACAATATATAAAGCCCCACAGAGCC 6351
QY 137 -----137
Db 6352 TTCTGCTTCTGCTCTCTCTTTGGAGACAGGGCTGCCAATTCATGTGAATGGCCACTTT 6411
QY 137 -----137
Db 6412 GCTCTAGATTCAGCCAGAGAACTTGTGGGTGATGATGAATAGGGTGTGGTTCGAAGT 6471
QY 138 -----Ile-----ValGlu-----140
Db 6472 GACTGGAATAATAGTTAAATGACAGCATTAATAGCACCTGCATATGTTGATTAATC 6531
QY 140 -----140
Db 6532 CAGTTAAAAAACGGTATTTCCCTGGTTCTGACCCAACTATATCAGTTTACAGAACACA 6591
QY 141 ---Ile-----141
Db 6592 CCATTCATGCTGAAGGACACATTAAAGAGTTTCTGTCCTTCTTCCAGTTAACAGG 6651
QY 142 -----Ser-----142
Db 6652 CTGGATCTGCAGCCGACTTATATTGCTTAGTAAAGCACTTTACAGTTGCATTTCATGAA 6711
QY 143 -----SerAsp-----144
Db 6712 GACATGAAGCGTCTTTGGCTGTTGTCGGGCTCCAATATATGATGCTCAGATTTGCAC 6771
QY 145 -----IleAsn-----148
Db 6772 TCTGAGTCATAATTACTTGGATCAATATGCTACTTCAATAAACTAGACCAATTTTT 6831
QY 149 -----Glu-----149
Db 6832 GATAAATCTACAGGATGAATTACAGCACTTAAAAATGACAGATTAATACACAACT 6891
QY 150 -----Gly-----150
Db 6892 CGAAAAACAGTCGAGAGATGTCTACAGACTGAAGCACCTGCTCTTAGAAAATGGTTTC 6951
QY 151 -----Asn-----152
Db 6952 AACTTGGTTTATAACTGTGTAAGTAACTGCTAACCTTTACCATTCGCTTGTAGATGCAGAT 7011
QY 153 Ile-----Ser---Leu-----155
Db 7012 ATCCCTGTACGATGTGACTCCTGCTGATGTTAGGTCCTTCTTAATGACTTTCTCTCT 7071
QY 156 -----Thr---Ile-----158

Db 7072 CCTGACACTAAATTTGCCATATTTGGAGAGCTGCTTGTCTTTCAGCAGACTAACTAAAA 7131
QY 159 -----Ala-----159
Db 7132 CTTTTTACAGTTTAAAACTTTTAGTTAGTTACTGTTTTTAAAGATGCTGAAGAAAGTGAG 7191
QY 160 -----Thr-----160
Db 7192 TTTGAAGTTGAGGAGCTGCCCTACTCATTTACACTGGACAGTGTCTTGCAGATTTTGTAT 7251
QY 161 Gly---ArgPro-----Glu---Pro-----165
Db 7252 GGTAAAGGAGCCCAAGTTTCTAACACATACCATGAATTAATTCATCGCGTAAAGACTTG 7311
QY 166 -----Thr-----166
Db 7312 TTTATGAACACCTTATATCTTGAATATACAGTAGTGTTTTGTGAACTGCAAAAGTTGCAAA 7371
QY 167 -----Val-----167
Db 7372 GTGTTGACATTTCCAGCTTGTGCTGACTACTCTCTCTGTGTGTGCTCGTAGTAAAG 7431
QY 168 Thr-----TrpArg-----170
Db 7432 ACCAAAACTGTCAAAGTGGAAAGACAAATTTGCCAGTGAATCTTGGCTTAAGAAGCA 7491
QY 171 ---His---IleSer-----ProLys---Ala 176
Db 7492 TGGCATTTTATCAGTGAATCAGTAGTAACGATGATCAGGAAGAACCAAGCCAGCA 7551
QY 177 -----Val-----Gly-----Phe---179
Db 7552 TTTGATGTCATTGTTGACATCTTAAAGACTGGGCATGCTTCCAGAAACAAAGTTCACT 7611
QY 180 ValSer-----Glu---Asp-----GluTyr---Leu---186
Db 7612 GTGTCAACCACTCAGCTTGTGGTTCTGAGGAGAGAGCTGTTGATTCCCTGAGCCCATG 7671
QY 187 GluIle-----Gln-----189
Db 7672 CACATGCTGTGTCCCAATGCTCAGAGTAGTAAGGTTTTTCCGCTCTGTGAAAGCT 7731
QY 190 Gly-----190
Db 7732 GGCTGTATTACAGCTGCTTTGAACAAATCTGCTCTAAGACAGCGCATTAGTTCCTCTG 7791
QY 191 -----Ile-----191
Db 7792 TTGTCATGCCACACAGCAAAACATAGATAGCCCTGCAAGCATCTTGAAGGCTGTGCATTAT 7851
QY 192 -----Thr---Arg---Glu-----194
Db 7852 ATGTTTCAGACGCTCAACATTTAGAACTGAAAAACTAATGGAATAATGCTTTGAAGCACTT 7911
QY 195 -----Gln-----195
Db 7912 TTGATGTAATTCACGTGAATTTGAGTCACTTGATGTCCCAAGATGACATAAAAAATTTTA 7971
QY 196 -----SerGlyAspTyr-----Glu-----200
Db 7972 AAGTCCCTCCCATGCTACAAATCCATCAGTGGCGCTATATGAGCATTTGCAAAATTTGGA 8031
QY 201 ---Cys-----SerAla-----203
Db 8032 ACGTGTATGTGCTTACCAAAAGTATTCTTCCAGCTGAAGTGGAAAAATGGACACAGTCA 8091
QY 204 -----Ser-----204
Db 8092 TCCTCTTCGCGTTTCTTGAAGAAAGGTGCATTTAAAAAGAACTCTATGAGGTGCTTGGC 8151
QY 205 -----Asn 205
|||

Db 8152 TGTTGCCAGTAGATCTGGAGGTGATTTGAACATCTTCTGCAAAAATTGAAAT 8211
QY 206 -----Asp-----Val-----AlaAla----- 209
Db 8212 CTCTCTTATGATGCAAGTTGGAGCAGCTGATTTATCTGAAGATAGACTGGCAAGATC 8271
QY 210 -----Pro-----ValVal 212
Db 8272 GAGGAACCGTCCAGAGATTAAAGGCAACTTTTGAAGAACTGGAAAGCTTATTTGATTATC 8331
QY 213 -----Arg-----ArgVal 215
Db 8332 CACGATGCCAACAATCGACTAAAGCAAGCAAAACATTTCTATGACAGAACTGTGAGATT 8391
QY 216 -----Lys-----Lys----- 216
Db 8392 TTTGAAGTTATGCTTCTGAAAAATTGTTTATCTTAAGGAGTTCTTTAAAAAAATGGAA 8451
QY 217 ---Val---Thr-----Val----- 219
Db 8452 CAAGTAATCAAACTTAAATAATCAAGCTGCAITTTATGACGTCTCGGTGGAAATTTTGAGA 8511
QY 220 Asn-----Tyr----- 221
Db 8512 AATATTGGACTGAAGTACCGCTCTCCAGCAGCAGTTGTTACAGTTTGGCCAAAGGAATC 8571
QY 221 ----- 221
Db 8572 AGTGTAGGGGCAATACAGAAAACTGGTCTAAAGAAACCTGCCAAGTACAGTTGCACATC 8631
QY 221 ----- 221
Db 8632 CTCTCCATCACAATTCGAAGAACGAATGGATTTGTTATCTGAAAAATTTCTGAAGAA 8691
QY 222 -----Pro-----Pro-----TyrIle----- 225
Db 8692 CTGTCTTAATACCATTCTTGTCCTGAAACGGGCCCGCTGAGTACATTCGGTTTCAC 8751
QY 226 -----SerGluAlaLysGlyThrGlyValPro-----Val-----Gly-----Gln 237
Db 8752 CCTCAGTACCAGGAGGTAAACGGAACA--CTTCTCTTATAAAGTTCAATGGAGCACAA 8808
QY 238 -----Lys-----GlyThrLeuGln-----Cys----- 243
Db 8809 GTGAATCCAAAGTTCAGCAATGTGATGTACTCCAGTCTGCTGGACATCTTGCCCTATT 8868
QY 244 -----Glu-----Ala-----Ser-----Ala----- 247
Db 8869 CTTCAGAGAAAGCCACACCGTTGAGCATTAAGAAACAGAGGAGTGCCTCGCTCCA 8928
QY 248 -----Val-----Pro----- 249
Db 8929 CAGGAACAGCTTGAACAAGTTTAAATATGCTTAATGTATACCTGGACCCCGCTCTTGAT 8988
QY 249 ----- 249
Db 8989 AAGTCAATTAATTCAGAAACATATGCAACATAACAATTTGGATGAGGAATGGTA 9048
QY 250 -----SerAlaGlu----- 252
Db 9049 AAAACTAGACAAAGGCTCTAAGGAGCATATATGAATTTCTGAGTGCAGAAAACAGAGAG 9108
QY 253 -----PheGln-----Trp----- 255
Db 9109 TTCGGTTTTACGCTTCGGGGTGTGGCCTTTGTAATGTTAGAGACGGATGGAAACTTCG 9168
QY 256 -----TyrIys-----Asp----- 258
Db 9169 AAGCTGAGGAAGTAGTAATAACCTGGAGTATGAGGCTGATTTTAAACCTTATCTGTAC 9228
QY 259 -----Asp 259
Db 9229 AAGTGCCTTTAGAGCTTGGACCTTTTTCATCAGCTGTTCAACATTTAGGTACTGAAGAT 9288

QY 260 -----Lys-----ArgLeuIle-----Glu 264
Db 9289 ATCATTCCACTAAGCAATATATGTTGAAGTGTAAAGCGA--ATATTCAAAGCTCTGAA 9345
QY 265 GlyLys-----Lys-----Gly----- 268
Db 9346 GGAAAGCAGTAGACCCTTAATGAATGCTGACAGTTAAGAGAGTGGTTTCTGCGCTATTTC 9405
QY 269 -----ValLysVal-----GluAsn-----Arg----- 274
Db 9406 AAGAGTCTACAAAATGATTCAGTCAAGGTGAGGAGTGCCTGGAGAAATGCCGGGACCTC 9465
QY 275 -----Pro-----Phe----- 276
Db 9466 GCACCTACCTTCCAAAGCCAGGATGGGAAGTTGGTGAAGTCAAGCATCTTGGTGTTCGAT 9525
QY 276 ----- 276
Db 9526 GATCGCCACATTATAAAGTAGGATCCAGGGGAATATTTGGGTGCAGATGCTAGTTGAT 9585
QY 277 LeuSer-----LysLeuIle----- 281
Db 9586 CTTAGCCAGTCTACTTAGGGAAGACCATGGATTTTCACACTAAGCTGATTAATGCTCTTT 9645
QY 281 ----- 281
Db 9646 CCTCAAAAGCTTCGACCTCGTCTGCTGAGCAGTATACTTTGAAGAGCAGCTTGTATGAGGAG 9705
QY 281 ----- 281
Db 9706 ACCCTAAGTGTCCAGTTTGGCGCATTTGTCTCTTTCAGGGAAGACTCGAGCTTCTC 9765
QY 281 ----- 281
Db 9766 TTGTCTTCAGAGCAGTTTCATCACAGGACTCATTCGAATCATGAAGCATGAAAAATGATAAT 9825
QY 281 ----- 281
Db 9826 GCTTCTCGCCANTGAAGAAAAGCCATAAGACTTTGCAAAAGCTCTAAGAGAAGGGCTG 9885
QY 282 -----Phe-----PheAsp-----Val 285
Db 9886 AAAGTTTCTCTGTTTGTGAAGCTTCAGACAACATTAAGGGTTAAAGGTTTTTAATCTTATT 9945
QY 286 -----SerGlu----- 287
Db 9946 CCCCATAGCAGGAGTGAACCTTTGCTTTTCTAAAGCGATTTGGCAATGCAGTCACTCTTG 10005
QY 288 -----His----- 288
Db 10006 CTCTACATCCAACTTCAGACAGCAAGACATTAACTTTCTGTAGCTTAGCGATGACACA 10065
QY 289 -----Asp-----Tyr-----Gly 291
Db 10066 CTTAAATCAGCAACTGACATTTGATTTCTGACACGCTCATCTTAATTCGTATGCTGGGA 10125
QY 292 ---Asn---Tyr-Thr-- 294
Db 10126 TGCAATGACATTTACAGGATCAGTGAAGCTTGACAGTTTAGGGGTGAATACGACTCC 10185
QY 295 -----CysValAla-----Ser-- 298
Db 10186 TCTGAGCCATCAAACTGGAACCTCCCATGCTGGCACACCAATACCCGCTGAGATCCAT 10245
QY 299 -----AsnLysLeu----- 301
Db 10246 TACACACTACTTATGATCCAATGAATGTTTTTATCTCTGGGGAATATGTTGGTTACCTT 10305
QY 302 -----GlyHisThr----- 304
Db 10306 GTGATGCTGAAGTGGTGTATCTATGGTTCATACCAACCAACATACACATACGCAATT 10365

QY 304 ----- 304

Db 10366 ATTGTGCAAGATTCAAGAGAGAGTGTGACAACTAGTCTTCTTAGAAAGATCTAT 10425

QY 304 ----- 304

Db 10426 CAGATCGATATTGGCTACAGTGAATATAAGATAGTCAGCTCTCTTGATCTGTACAAGTTC 10485

QY 304 ----- 304

Db 10486 TCAGGCCCTGATGAAGCTCCCAAAACAGAGAGAGTGTCCCAACCAACCAACAGGCC 10545

QY 305 ----- 307

Db 10546 ACCGAATCTGACTCTGCTGCTGAGAGCATCCCTCTCTTCTCTGCGAAGAGAGC 10605

QY 308 ----- 310

Db 10606 CACAAGTCTCCCTCCACCAACACCAATTCCTCCCAAGAAAGCTCAAGGTGAATCTTTACCA 10665

QY 311 ----- 311

Db 10666 GAAATCTTAAAGAGTGCATCAGTGTGGAGCAAGCTTGAAGCTTCCGAATCAGAG 10725

QY 312 ----- 312

Db 10726 CGGAAAAGATCATTAGACGCTGTGATTTGAAGTGGCACCTCGACAAAATCCAGAAAT 10785

QY 312 ----- 312

Db 10786 CAGTATATTGCTTAATGAAGTGTTCAGCACCTGCGAATGAATCAACAGATTAGAAAA 10845

QY 313 ----- 313

Db 10846 CAGGCTTTCTCGATCAAAATGCACAGAGCTTCAAGAGAACATTTCAACCTCTGCA 10905

QY 314 ----- 317

Db 10906 TCTGATTTCACTCAGACAAGTACTCATTTCAAGATTTTACACTTCGTGGA---ATCAA 10962

QY 317 r-----GluValSerAsn-----GlyThrSer-----Arg----- 325

Db 10963 GAAGCCACAGTCTATAATCTGAAGGCAACAGCAAGCAAGAAAGAAATGCCCTCTCT 11022

QY 326 -----Arg-----Ala-- 327

Db 11023 GCTGGACAGACATACTCTCAAGGTTCTTGTCTCCACCTTCAAGTCAAGTGGGCAAT 11082

QY 327 ----- 327

Db 11083 CCAGTGAAGCCCGGAGATGGTTAAGACAAGCCAGAGCAAACTTCTCAGCTGCCAGGAAT 11142

QY 328 -----GlyCys-----Val-----Tr 331

Db 11143 GACCTTCACAAAATGCCAATCAATGGTGTGCTTCAAGTGTATCTTCCACCAAGCTG 11202

QY 331 Pleu---Leu---Pro---Leu-----LeuVal-----Le 338

Db 11203 GCTTGTGTCGCGCACTATGCTGTCTCAGGGGGAATCTGTATAAGATGTAAAGCCAACT 11262

QY 338 uHisLeu----- 340

Db 11263 GCATTGCAAAAGATAGAGGTACAGTCAGCAGCTGGAAGGACTGACAAACGATGTG 11322

QY 341 -----LeuLeu-----Lys-----Phe 344

Db 11323 CACACATTGGAAGCTTATGGTGTAGACAGCTTGAACCAAGTACCTGATTTGCTTC 11380

RESULT 11

AK028345

LOCUS

DEFINITION

CDNA, RIKEN full-length enriched library, clone:3732419F12

product: weakly similar to OPIOID BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR (OBCAM) (OPIOID-BINDING CELL ADHESION MOLECULE) (OPCML) [Homo sapiens], full insert sequence.

ACCESSION

AK028345

VERSION

HTC; CAP trapper.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Carninci, P. and Hayashizaki, Y.

REFERENCE

High-efficiency full-length cDNA cloning

AUTHORS

Mech. Enzymol. 303, 19-44 (1999)

JOURNAL

99279253

MEDLINE

10349636

PUBMED

10349636

REFERENCE

10349636

AUTHORS

10349636

TITLE

10349636

JOURNAL

10349636

MEDLINE

10349636

PUBMED

10349636

REFERENCE

10349636

AUTHORS

10349636

TITLE

10349636

JOURNAL

10349636

MEDLINE

10349636

PUBMED

10349636

REFERENCE

10349636

AUTHORS

10349636

TITLE

10349636

JOURNAL

10349636

MEDLINE

10349636

PUBMED

10349636

REFERENCE

10349636

AUTHORS

10349636

TITLE

10349636

JOURNAL

10349636

MEDLINE

10349636

PUBMED

10349636

REFERENCE

10349636

AUTHORS

10349636

TITLE

10349636

JOURNAL

10349636

MEDLINE

10349636

PUBMED

10349636

REFERENCE

10349636

AUTHORS

10349636

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>
URL: <http://fantom.gsc.riken.go.jp/>

FEATURES

source
1. 2798
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:3732419F12"
/db_xref="MGI:2350203"
/db_xref="taxon:10090"
/clone="3732419F12"
/tissue_type="embryonic body below diaphragm region"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"
65. 631
/note="unnamed protein product; putative
weakly similar to OPIOID BINDING PROTEIN/CELL ADHESION
MOLECULE PRECURSOR (OBCAM) (OPIOID-BINDING CELL ADHESION
MOLECULE) (OPCML) [Homo sapiens] (SWISSPROT|Q14982,
evidence: FASTY, 100%ID, 50.7%length, match=525)"
/codon_start=1
/protein_id="BAC25895.1"
/db_xref="GI:26390424"
/translation="MGVCGYLFPMKCLVVLVSLRLFLVPTGVFVRSQDATFPKAMDN
VTVQGSATLRCTIDDRVTRVWLNRSTILYAGNDKWSIDPRVILVNTPTQYSIM
QNDVYDEGPVTSVQDNPDKTSRVHLIVQVPMINISSDITVNEGSSVLLCLAI
GRPEPTVTRHLSVKGVFTMQSPKSLV"

CDS

ORIGIN

Alignment Scores:

Pred. No.: 9.95e-16 Length: 2798
Score: 1696.60 Matches: 244
Percent Similarity: 31.81% Conservative: 49
Best Local Similarity: 26.49% Mismatches: 24
Query Match: 70.46% Indels: 605
DB: 11 Gaps: 116

US-10-017-084A-523 (1-344) x AK028345 (1-2798)

QY	5	Gln	Pro	-----	LysMetHisAsnSerileSer	-----	TrpAlaIlePhe	17
DB	17	CAAGGACCTTGTCTGCAGG	---	AGT	-----	TCGGGAGTTGTGG	-----	CTG 58
QY	18	Thr	-----	GlyLeuAlaAlaLeu	-----	-----	Cys	24
DB	59	TCGAGAATGGGGTCTGTGGGTAC	-----	CTGTTCTCTGCGCTGGAGTGCCTCGTGGTC	-----	-----	-----	112
QY	25	-----	LeuPhe	-----	-----	-----	-----	36
DB	113	GTGTCTCTAGGCTGCTATTCTTGTATCCACAGGAGTGCCTGGCGCAGCGAGATGCC	-----	GlnGlyValProValArgSerGlyAspAla	-----	-----	-----	172
QY	37	ThrPheProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArg	-----	-----	-----	-----	-----	56
DB	173	ACCTTTCCCAAGCTATGGACACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGG	-----	-----	-----	-----	-----	232
QY	57	CysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyr	-----	-----	-----	-----	-----	76
DB	233	TGTACCATAGATGATGGGTCACTGGGTAGCTGGCTAAACCGCAGCACAACTCTCTAT	-----	-----	-----	-----	-----	292
QY	77	AlaGlyAsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThr	-----	-----	-----	-----	-----	96
DB	293	GCTGGGATGACAAAGTGGTCCATGACCCCTCGAGTGATCATTTTGGTCAACACGCTACC	-----	-----	-----	-----	-----	352
QY	97	GlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlnGlyProTyrThrCysSer	-----	-----	-----	-----	-----	116
DB	353	CAATACAGTATCATGATCCAGATGTGGATGTATACATGAGAGTCCATACACCTGCTCT	-----	-----	-----	-----	-----	412
QY	117	ValGlnThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerPro	-----	-----	-----	-----	-----	136
DB	413	GTGCAGACAGACAAATCACCCCAAACTCCCGGGTCCATCTCATATGTGCAAGTTCTCTCC	-----	-----	-----	-----	-----	472

QY	137	LysIleValGluIleSerSerAspIleSerileAsnGluGlyAsnAsnIleSerLeuThr	156
DB	473	CAGATATGAACATCTCGTCAGACATTACCGTGATGAAGGAAGCAGTGTGACCTGTGA	532
QY	157	CysIleAlaThrGlyArgProGluProThrValThrTrpArgHis	171
DB	533	TGTCTTGCATTTGGCAGACAGACCAACGGTGACATGGAGGCACCTGTCTAGTCAAGGT	592
QY	172	---Ile---	174
DB	593	AAGGTATTATTACATGCAAGTTTAAAGAGTGTACTTTAAAGCCGGCTTGGTTCTCATGC	652
QY	175	-----Lys-----	176
DB	653	TAAAGGAGATCAGTATCCAGAAAATAACATTTGATGTGAATGCATCAATACGCCATCTC	712
QY	177	-----Val-----	180
DB	713	AGGACCAATCTGTTTATGTATCTGCTGAAGTGCACCATTCAGGCAAGGAATTT	769
QY	181	SerGluaspGlu---TyrLeu	187
DB	770	GCAGAA---GAAAATTACCTAAATTAATCTGTCAGCTTTTCTTTCATGACTTGGGAAGCC	826
QY	188	---Ile---	189
DB	827	TTTGTTTTCAAACTGAAGGAAGAGTGTGTAGTAGCTTTTGTGTAGTAGTAGTAAGTTG	885
QY	190	-----Gly---Ile---	191
DB	887	TGTGGAGATGGATGTGCCCTTTCTTATGGTGGTGTGATCTTGACAGCATGCCCTGGGA	946
QY	192	-----Thr-----	195
DB	947	ACTTGACATTAATGATGTGTACTAAAGAAAACCATACCTGCTGTATTTTTCAGAAACAG	1006
QY	196	-----Ser---Gly---Asp---	200
DB	1007	TTTGTAGAGTGTATCTGTGGATCTGATGGGGGAAAGGTCAGTGGAGTGGGGGATT	1066
QY	201	-----Cys-----	201
DB	1067	GCATCTGCATGACCTTGTGGGTGTTTTCAGCAATTTGATTAACACATCAGTTACTACCA	1126
QY	202	SerAlaSer	206
DB	1127	TCCTCCTAAATATGAAGAAATCTAAAGGACATGGGTTCTTATCTCTCTTGGAAATAA	1186
QY	207	-----Val 207	207
DB	1187	ACTTGGTCCAACTTGAACCTTCAAGATGGGCACAGGCATCTGATATATATACACTGTT	1246
QY	208	Ala	212
DB	1247	GCAGCAAACTATGATTTGATTTCTTGAGATTATACAGGAATCAAGTCTCCTCAGGCAAT	1306
QY	213	Arg	215
DB	1307	AGAAACACAAAGGTGAACCCAGTGTAGTAAATATACATATGCTGTGTGTATATGA	1366
QY	216	Lys	218
DB	1367	AACTAATGCATCTCAAGAAAGCAAGGGACTTAATCTCTCASTAACTTGAAGAAGCA	1426
QY	219	-----Val---Asn---TyrPro	222
DB	1427	GAGATCTCAAAATACAAATTTCCCTCCCTGAGAGGAAAGAAACAATAACAGACTTG	1486
QY	223	-----Pro---Tyr---	228
DB	1487	CTTGAGCTTCCAGGGTGGCTCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1543
QY	229	LysGly-----ThrGlyValPro-----Val---GlyGln---	237

QY 12 Ile-----Ser----- 13
DB 219 ATCGTTAGTCATTTAGACGATGAATCTGAAGCACAGCTTCAGAAATTTTGTAGCAGCAT 278
QY 14 -----Trp-----Ala 15
DB 279 TGTACAAAACCTTGAGGGTTTGCTTTAAAAAATTAGATCATCTATACAAACATCCGCT 338
QY 16 -----Ile-----PheThr-----Gly----- 19
DB 339 TATTAAAAAATATATCTTACCATTACCAAGTCTGTTTTGCAGATAATGGAGAAGAT 398
QY 20 -----LeuAla-----Cys----- 24
DB 399 GCCATTGCGAAATTTGTAAATCAAAATTAACCTTCTGATCAGGGAATTTCTCTTATACAA 458
QY 25 -----Leu-----Phe-----Gln----- 27
DB 459 GAGGAAGTTCTTGCTAGTTTAAACCGTAGCAGTGAGAAAGAGAAAGAAATATTATCAAGA 518
QY 28 -----Gly-----Val-----Pro----- 30
DB 519 ATTGGCAATATTCAAGCGCATTAACCATCTCTGATCAGGGAATTTCTCTTATACAA 578
QY 31 Val----- 31
DB 579 ATTGAAGGTTGTAAAGTCTTACACCATCTGCTCCAACTCCAGCAGATCTCGACTTTC 638
QY 32 -----Arg-----SerGly----- 34
DB 639 TATTTCAGTAATAGACAGTAGTAGAGCTACTTAATTCGTCCTGCGAAACATGTTGAAAT 698
QY 35 -----Asp-----Ala----- 36
DB 699 AGAAGCTTAAAGACCACTAGCTGCTTAAAGCTTGTTTTAAAGATATTGAATGCAAT 758
QY 37 ThrPhe-----Pro----- 39
DB 759 TTATTTCATGAAGAGGTAACACAGCTTATGTTATGGTCTCTTGAGAATCTATCTCTCT 818
QY 40 -----Lys-----Ala-----Met----- 42
DB 819 TAAAAATGAGAAATCCAAATGTGCTTGAGTGTAAACACCATTAATAATTCACAGATATC 878
QY 43 -----Asp----- 43
DB 879 ACAGAACAGATGGTATCAGCTGTGTGAACCTTTTGACCTGATATAGAAGTACTAAAGGA 938
QY 44 -----AsnVal-----ThrVal----- 47
DB 939 TCTCTTTTGAATGAAGAGAACCTTATTTCCCACTCTCAGTTTACCTCACAGATAT 998
QY 48 -----Arg-----Gln----- 49
DB 999 TCTTCACTCTTAAGACAGATTTGTTTAAAGAGAGAGCAGCTCTCAAGAAAGGATGT 1058
QY 50 -----GlyGlu-----SerAlaThr-----Leu-----ArgCys 57
DB 1059 TGTGCAAGTGGCAAAAAAATTTGAAGCTTTACAGGTCGGTCTGTCTGATCAAGATGT 1118
QY 58 ----- 58
DB 1119 TCTTCTGAAGAACCCAAACCTCTTACTGGTTTAAATAAGAAATCACACACTGTGTGCA 1178
QY 59 -----Ile-----Asp-----Asn----- 61
DB 1179 ATCATCTGAAGGAAGATGACATTGAAGAAAATAAATGGTTCCAGCCTGCAGGAAG 1238
QY 62 -----Arg-----Val 63
DB 1239 GCCTCCAAATATTCCAGGCTCTTGGTCTGMAAGGAGATCTCTGTAACTCTGTGACC 1298
QY 64 ThrArg--Val-----Ala-----TrpLeu----- 69

DB 1299 ACCAGATATGTGTGATGTAGSCCATGCAATCTCATTTGGCTCCTCACTTCTCTTGTGTA 1358
QY 69 ----- 69
DB 1359 AAGTATCCATGTAAACCTGGAAAAAGCAATTAGGATCTTCACAAAACCTAGCCTTAGTGC 1418
QY 70 -----Asn----- 70
DB 1419 TGCTTAAAAACACTTTAAAAATTTGTGTGTGATTTCTTCAAAAACCTTTAGTGAGA 1478
QY 71 Arg-----Ser-----Thr-IleLeu-----TyrAlaGly----- 78
DB 1479 AGACTACTATCAATTCAGCATATTTTGTCTTGAGATTTAC---GGATTTCATGCATGATCA 1535
QY 79 ---Asn-----Asp-----Lys-----Trp----- 82
DB 1536 TCTAAATGAAGGGAAGAAATTTCTTTAGAGCCTTAAAAATTTCCATGGGTTTGGACTGGCAA 1595
QY 83 ---Cys-----LeuAsp----- 85
DB 1596 AAGTTTTTGTCCACTTGCCTCCAGGCTGTGATTAACCAATCAATGATCTTGACCTTCAGCC 1655
QY 86 -----Pro----- 86
DB 1656 TTATTTGCATAATGTACTAAACCACTGCGAAAAATTCACCAACTATTTAAGGTCCTGG 1715
QY 86 ----- 86
DB 1716 TTCAATAGAGGTTGACATCAGATCATATTTCCATGGTTATTTCAGAAGATATATCTCAA 1775
QY 86 ----- 86
DB 1776 AAGTGACCAAGATCTCAGTGAAACAAGAAAGCAAAATCTTCATCTTATGTTGAATAT 1835
QY 87 ---Arg----- 87
DB 1836 TATCAGATGGCTGTATAGCAATCAGATTTCCAGCAAGCCCAACACACACAGTTCCTATACA 1895
QY 87 ----- 87
DB 1896 TCATAGCAAAAATCTCTTAACTTATCATGAAGCCAAATTCAGAAATGCTGTTATTGTGA 1955
QY 88 -----Val-----Va 89
DB 1956 CATTAAAGTTGATGACCTTAATGACTTACTTTGAAGATTCTGTGGAAACCAATCATTTTGGT 2015
QY 89 |-----Leu-----LeuSer----- 92
DB 2016 GCATGAGGACATACCCATGAAAACCTGCAGAAATGGCTTAAAGTTTCCATGCTTAGTACAAG 2075
QY 93 -----AsnThr-----GlnThr-----Gln----- 97
DB 2076 ACTGATAAATCTCTGAATAACATGGGATTTGAGCAGTCAAGACAAAGAGAGCCACTTACTGT 2135
QY 98 -----Tyr-----Ser-----Ile----- 100
DB 2136 AAGAATTTAAAAATATTCTGGAAGATACCTCTTCAGTGTCAAGATATTTTAAAGAACTACT 2195
QY 101 -----Glu----- 101
DB 2196 TCAAAACGCTGATGATGCAAAATGCAACAGAAATGCAAGTCTTCTTGTGATATGAGAAGAA 2255
QY 102 -----Ile----- 102
DB 2256 TATGGCAATAGAGAGAATCTCTAGACCCAGGATGGCAGCTTGTCTATGGACCTGCTT 2315
QY 103 -----Gln-----Asn----- 104
DB 2316 GTGGTCAATCAACAATTTCTCAATTTCTCAGATTCAGATTTTGTGAACATAACTAGGTAGG 2375
QY 105 -----ValAsp----- 106

Db 2376 AGAATCTTTAAAGGGGAGAGTTGACAAAGTTGGAAATTTGGTCTTGGATTTAATTC 2435
Qy 107 -valTyr-----Asp-----Glu----- 110
Db 2436 TGTGTACCATATCACTGACATCCCATCAATPATAGTCGGGAATTCATGATAATGTTTCA 2495
Qy 110 ----- 110
Db 2496 TCCAAACATAAATCATATCAGTAACACATATAAGACAAATCCAAATCCTGGGATCAAAAT 2555
Qy 110 ----- 110
Db 2556 TAATTGGAGTAACAACAGAAAAGACTTAGAAAATTTCTTAATCAGTTCAAAACCAATTTAT 2615
Qy 111 -----ProTyr----- 113
Db 2616 AGATGTAATTGGCTGTGAGTTACCTTTGACTGTGTAGAAGACCTTTACAGCTATAATGGAAC 2675
Qy 114 -----Th 114
Db 2676 CCTTTTCGACTGTCTTTAGAACTCAACAGGAAGCAAAAGTGAAGTGAAGTTAGTAGTAC 2735
Qy 114 rCyS-----Ser--Val----- 117
Db 2736 GTGCTCAATACAGCAGATATTTATTTCTTTGTGGATGAATTTAGTCTCTGTGGACACAG 2795
Qy 118 -----Gln----- 118
Db 2796 GCTTATCATTTTCACTCAGAGTGAAGTCAATGTATTTGAAGTACTGTGAATTGAGGA 2855
Qy 119 -Thr-----Asp----- 120
Db 2856 AACCAACCCAGTTTAGCACAAGATACAGTAATAATTAATAAATAATCCTGCTCTTCCAA 2915
Qy 120 ----- 120
Db 2916 AGCAATTGAACACACTGTCTTAAGTGTTTTAAAGAGGCTGCTAAGCTCATGAAGACTTG 2975
Qy 121 -----Asn----- 121
Db 2976 CAGCAGCAGTAATAAAGCTTTCCAGTAGTGAACCAAGTCATCTTGCAATCTTCAGAT 3035
Qy 122 -----His----- 122
Db 3036 CACAGTGAAGAATTTACCATGTGTTTCAAGAGATTGCTGATTTACAGTCGCCACTTTT 3095
Qy 122 ----- 122
Db 3096 TAGAGTCCAGATGATGACCCAGCTGCTCTCTTTGAAATGGCTAAGTCTGGCCAAATCAA 3155
Qy 123 ---Pro-----LysThr----- 125
Db 3156 AAAGCCATCAGATGAGTTGTCACAGAAAACAGTAGAGTGTACCAGTGGCTTCTGTGTAC 3215
Qy 125 ----- 125
Db 3216 TTGCATGACACAGGAGGCTCTGAAGTTTTCCTGAGTGAGAGTGAAGAAGACTAGG 3275
Qy 126 -----Ser----- 126
Db 3276 ACTGGTTCCATGTGGGCGAGTAGGAGTTACGCTGTGCAAAATCCAGGACCAAGAGTGGAC 3335
Qy 127 -----Arg----- 127
Db 3336 AGTGAACACACATTTGAGAGGTTTGTCTATTACCTTTACGAATAAACAAGGCTT 3395
Qy 128 ---ValHisLeu----- 130
Db 3396 GCCAGTTTCATATCAATGGGTCTTTGCTGTTTACATCAATAGGAAGAAATCTGGAAGAC 3455
Qy 131 -----IleVal----- 132
Db 3456 AGATACAAAGGCGATGGAATACCAGTTCATGAGACATGTTTATGTGAAAGCTTACTT 3515

Qy 133 -GlnVal-----Ser----- 135
Db 3516 ACAGGTACTAGAGTGTCTTACGGACCTGCCACTAGTGGGAGCTAATGGATTATACTTA 3575
Qy 136 -----Pro-----LysIleVal----- 139
Db 3576 CTATGAGTATGCCCCGATCCTGATTTAGTTTCTCATGATGATTTTCTGTAAATTTGCCAAGG 3635
Qy 140 -----Glu---Ile----- 141
Db 3636 ATTTTATGAAGATATAGCTCATGAAAAAGGAAAGAACTGACCAAAAGTCTTCTCTGATGG 3695
Qy 142 -Ser-----Ser-----Asp---Ile----- 145
Db 3696 ATCTACTGGGTTTCCATGAAGAACGTAAAGATTTCTAGATGACTCTATACTTTAAAGAAG 3755
Qy 146 -----Ser-----Ile----- 147
Db 3756 AGATGTTGGTTCAGCAGCCTTCAAGATATTTTGAATACCTCAAGAAGACTGGGTCCAA 3815
Qy 148 -Asn-----Glu---Gly-- 150
Db 3816 AAACCTTTGTGCTGTGAACCTTCTTCTCGGTAAAAATTAGGATTTGAAGAAGCTGGCTG 3875
Qy 151 -----Asn----- 151
Db 3876 CAAACAGATACTACTTGAATAACACATTTTCAGAGAAACAGTTTTTTTCTGAAGTGTTTTT 3935
Qy 152 ---AsnIle----- 153
Db 3936 TCCAAATATTCAAGAAATTTGAAGCAGCACTTAGAGATCCTTTTAATGATCTTTGTTCTAAA 3995
Qy 154 -----Ser-----Leu-----Thr---CysIle-----AlaTh 160
Db 3996 TGAAGAAGTTGAGAGTTCTCGGAGTTCTTCTGTGTACTCCATGATTTCTTGTTCCTT 4055
Qy 160 r---Gly-----Arg-----ProGlu----- 164
Db 4056 GGAGGGGCATCCTTTGGTTTGGCCATCAAGATGTCCACCCCGAAGGAGGAGTTCGAAA 4115
Qy 165 -----Pro-----Thr----- 166
Db 4116 GTTATTTGTATTTAAAGATGGGAGATTCCTTATGTTTCTACTCAGGATTTATCTCAATCC 4175
Qy 167 -----Val-----ThrTrp----- 169
Db 4176 TATTATTTGATTAATACTAGTTCAAGTTAGTATGGCAAAAGATGATATTTTATGGGATGA 4235
Qy 170 -----Arg-----His----- 171
Db 4236 TATGCTAGAACGTCGACGTGTCAGTACTGAAATTAATAAAGATGATCATCTTCTGTCATG 4295
Qy 172 -----Ile-----Ser-----Pro-- 174
Db 4296 CCTAAGAAGTAGTATCTTATTTGAGTCTTATCCGATGAGAACTAAAAATAAGGATCCTAG 4355
Qy 175 ---Lys-----Ala-----Val----- 177
Db 4356 AGCAAAAGGATTTTGGTGCAAAATATCAAAATATCCGCTTCTTCCATTTCTGCAAAACC 4415
Qy 178 ---GlyPhe---Val-----Ser-----Glu----- 182
Db 4416 AGCAGGTTTCTTGGACTGGGAAGGCAACAGTTTAAAGCTGAAACCATGTTTGCAGC 4475
Qy 183 ---AspGluTyrLeu---Glu-----Ile-----Gln----- 189
Db 4476 AACTGACCTTTATACAGCTGAACATCAAGATATAGTTTGTCTTTTTCGAACCAATTTCTAAA 4535
Qy 190 -----Gly---IleThr-----ArgGlu----- 194
Db 4536 TGAATAATCCCATCTTTTAGAGGTTGTGTTTCAGTGTCTATTTAGGCTGTTTAAAGAGTTTTT 4595

QY 195 -----Gln----- 195
Db 4596 GGGATTACTCAAGAAGCCAAAGTTGATCTGGTTATAAACCAGTTGAAAGAAGTAGCAA 4655
QY 196 -Ser--GlyAsp-- Tyr--Glu-----Cys----- 201
Db 4656 ATCAGTTGATGATGGAAATTACACTGTACCAGGAGAAATATCACCAGTCTGTCTACAAATA 4715
QY 202 -----SerAla----- 203
Db 4716 CCTTCATGAAGCCTTGATGCAAAATGAAATCACTAAGATGTCATTAATTGATAAGTTAAA 4775
QY 204 -----Ser-----Asn-----Val----- 207
Db 4776 ACCCTTTAGCTTCATCTAGTTAGAAATGCATATGTGACTCAGAAAAGGTTTCTTTTCA 4835
QY 208 -----AlaAlaPro----- 210
Db 4836 TTTAAATTTTGAGCGGCACCATACCTTTATCAGTTGCCTTAATAAGTATAAAATAATTT 4895
QY 211 -----Val--ValArg----- 213
Db 4896 CCGGCACTTTTGAACCGTGGGTGTGAGGCACTCATGCACCTGTTGAAGATTTTGCTCT 4955
QY 214 -----Arg--ValLys--ValThr----- 218
Db 4956 TGTTTGGAACTTATTCATCAAGAAGAGGAAACAAATACAGAAAGAAATTTTCA 5015
QY 219 -----Val-----Val----- 219
Db 5016 GCCTTGGCGGCAATATCAGTGAAGNATATGAGTCTCATTTAGAGAAAGAAACAAGA 5075
QY 220 -----AsnTyr-----Pro-----Pr 223
Db 5076 ATTTTGTGAGAAAATATGCAAGATATTATTCGAGATACCTTAATCTTATGCTTCTCCC 5135
QY 223 o-----Tyr-----Ile-----Ser----- 226
Db 5136 TGCTAAATCGTTATGCTACAATGATGTCCTTGGATTAAGATTAAGGATACCACTGTAAA 5195
QY 227 -----Glu-----Ala----- 228
Db 5196 ATATGTGATGCTGACATACCAGGGAAGTAGCAGTAAACCTAGAGCAGTCCCAAGCG 5255
QY 229 -----Lys-----GlyThr----- 231
Db 5256 ACACAAAGCCTTAGAAGATATGCATCCAATGCTGTGTTTACACACTTGGCAGCAAAAT 5315
QY 232 -Gly----- 232
Db 5316 TGGCGAGAAAGAAAATTCACCAGCAGAAATTAAGAGCATCCTTAATGCATATCCTTCTGA 5375
QY 232 ----- 232
Db 5376 AAAGGAAATGTTGAAAGAGCTTCTTCAAAATGCTGATGATGCAAAAGCGCAGCAAAATCTG 5435
QY 233 -----Val-----ProVal----- 235
Db 5436 TTTTGTGTTGATCCTAGACAGCATCCAGTTGATAGAAATATTTGATGATAAGTGGGCCCC 5495
QY 235 ----- 235
Db 5496 ATTGCAAGGCCAGCACTTTGTGTGTACAAACACAGCCATTTACAGAGATGATGTAG 5555
QY 236 -Gly--Gln-----LysGlyThr----- 240
Db 5556 AGGAATTCAGAACTTGGAAAGGCACGAAAGAGGAAATCCTTATAAACTGGACAGTA 5615
QY 240 ----- 240
Db 5616 TGGAAATAGGATTCAAATCTGTGTATCATATCACAGACTGCCATCTTTTATTTCTGGCAA 5675
QY 240 ----- 240

Db 5676 TGACATCCTGTGTAATTTTGTATCTCTCATGCCAGATATGCACCAGGGGCCACATCCATTAG 5735
QY 241 -----Leu-----Gln----- 242
Db 5736 TCCCGAGCGCATGTTTAGAGATTTGGATGCAGATTTTAGACACAGATTTCTCAGATGTTCT 5795
QY 243 -----Cys----- 243
Db 5796 GGATCTTTATCTGGGAACCCATTTAAACTGGATAATTTGCACAAATGTTCCAGATTTCTCT 5855
QY 244 -----Glu--Ala-----SerAlaValPro----- 249
Db 5856 TCGTAATGCAGAAATGGCAAAAGTTTCGGAAATTTTCGTCTGTCTCCAGCATTCAGACAGAA 5915
QY 250 -----Ser-----AlaGlu----- 252
Db 5916 GGTCCAGAAATCTTTTGGACAAACTGCGCTCAGATGGGGCAGAACTTCTAATGTTCTTAA 5975
QY 252 ----- 252
Db 5976 TCACATGGAAATAATTTCTATTGTTGAAATAGATAAGAGTACTGGAGCTCTAAATGTGCT 6035
QY 253 -----Phe----- 253
Db 6036 GTATTAGTAAGGGCAAAATCACAGATGGAGACAGATTTGAAAAGGAAACAATTTCAATGC 6095
QY 254 -----Gln-- 254
Db 6096 ATCTGTAATGATAGTGTGTACTAAAGAGCGCAGCTCAAGACATACCACTTCAACAAAT 6155
QY 255 -----Trp----- 255
Db 6156 AACCTATACATGATGACTGAGGACTCTGAAGGAAATCTTACTACGTGGCTAATTTGTA 6215
QY 255 ----- 255
Db 6216 TAGATCAGGCTTTTCAAGTATGGAGAAAGTATCTAAAGTGTCTATATCAGCTCAACAGAA 6275
QY 256 -----TyrLys 257
Db 6276 CCAAGATATTAATCTTTTCCACGCTGGTGGTAGTGCCTGCACTTACTCACAATATAA 6335
QY 257 s----- 257
Db 6336 AAAACCCCATAGGCGCTTCTGTTTTTGGCCTCTTTCTTTGGAGACTGGGCTGCCAATTTCA 6395
QY 258 -----AspAspLys-- 260
Db 6396 TGTGAATGGCCACTTTTGCACTGGATTCAGCAGAGAGAAACCTGTGGCGTGATGATAATGG 6455
QY 261 -----Arg-----LeuIle----- 263
Db 6456 AGTTGGTCTTCGAAGTGACTGGAATAACAGTTTAAATGACAGCATTAATAGTCTCTGCATA 6515
QY 264 -----Glu-----GlyLysLys-----Gly----- 268
Db 6516 TGTTGAAATGCTTAATACAGTTTAAAAAAGCGGTATTTCCCTGGTCTGTGATCCAACATATC 6575
QY 269 -----ValLys----- 270
Db 6576 AGTGTACAGAACACCCCTATTCATGTTGTTGAAGAGACACTTAAAGAGTTTTATCGTT 6635
QY 271 -----ValGluAsnArg-----Pro----- 275
Db 6636 TTTCCAGTT--AACCGTCTTGATCATACAGCCAGATTTATATGCTAGTGAAGCACT 6692
QY 276 -----PheLeu----- 277
Db 6693 TTACAATTCATTCACAGACATGAAACGCTCTTTTACCTGTGTGGCGGCTCCAAATAT 6752
QY 278 -----SerLysLeu-----Ile----- 281

Db 6753 TGATGGCTGACCTGCACTCTGCAGTTATAAATCTTGGATCAATATGTCTACTCTAA 6812
QY 282 -----PhePhe-----AenVal-----SerGlu-----His----- 288
Db 6813 TAAACTAGACCAATTTTGGCAATTTACTACAGGATGAAATCAACACACCTTAAATATGC 6872
QY 289 -AspTyr----- 290
Db 6873 AGATTATAATATCAACACACGCAACAGTAGCAGAGAATGTCTATAGGCTGAACATCT 6932
QY 291 -----Gly-----Aen-----Tyr-----Thr----- 294
Db 6933 CCITTTAGAAATGGTTTCACTTGGTTTATTAATCTGTGATGAACCTCTAATCTTTACCA 6992
QY 295 -Cys-----Val-----Ala----- 297
Db 6993 CTGCTTATAGATCAGATATCTCTCTCTGACATTAATGGCAATATGGGAAGCTGCTTGTCTCT 7052
QY 298 -----Ser----- 298
Db 7053 TTTAATGACATTTTCTCTCTCTGACATTAATGGCAATATGGGAAGCTGCTTGTCTCTCT 7112
QY 299 -----Asn-----LysLeu----- 301
Db 7113 GCAGCAGACTAATCTAAACTTTTTCATAGTTTAAACTTTTGTAGTTGATTATTCTTTAA 7172
QY 302 -----Gly----- 302
Db 7173 AGATGCAGAGAAATGAGATTGAAGTTGAGGATGTCCTCTCATCACATGAGACAG 7232
QY 303 -----His----- 303
Db 7233 TGTTTGCAAACTTTTGTATGCAAAAGCCCAAGTTCTTAACAATATCAATGAATTGAT 7292
QY 304 -----Thr----- 304
Db 7293 TCCATCCGCAAGACTTTGTTTATGAATACATATATTTTGAATATAGTATATTTTATT 7352
QY 305 -Asn-----Ala-----SerI1 308
Db 7353 CAACCTGTAAGTTGCAAAAGTTTGTGACATTTCCAGCTTTTGTGATTTTGTCTCTGT 7412
QY 308 eMet----- 309
Db 7413 GTTGCTCGAATATAAGACCAAAAGTTGCACAAAGTGGAAAGACATTTTGAAGTGA 7472
QY 310 -----Leu----- 310
Db 7473 GTCTTGGCTTAAGATGATGATGATTTTATTTAGTGAATCTGTAAGTGTGAAGAAGATCA 7532
QY 311 -----Phe-----Gly----- 312
Db 7533 GGAAGAAACAAACCAACATTTGACATTTGATGATCTTAAAGACTGGGCAATGCT 7592
QY 313 -ProGly-----AlaValSer-----Glu-----Val-- 319
Db 7593 TCCAGAACAAAGTTTACTGTTTTCAGCCCAACAGCTTGTGGTCTCTGAAGGAGATGTTCT 7652
QY 320 -----Ser-----Aen----- 321
Db 7653 GCTTCTCTCAGCTTATGACATTTGACATTTGACATTTTCCAAATGCCAGAGTGAATAAGTTT 7712
QY 322 -----Gly----- 322
Db 7713 TCATGCTCTAATGAAGCTGGCTGTATTTCAGCTTGTGTTGAACAAATCTGTTCCAAAGA 7772
QY 322 ----- 322
Db 7773 CAGTGCAATTTGTTCTTGTGTCATGTCACAGCAATATAGAGAGCCCCACAAGCAT 7832
QY 323 -----ThrSer-----Arg----- 325
Db 7833 CTTGAAGGCTCTACATTATATGTTCCAAACCTTCAACATTTAGAGCAGAAAAATTTAGTAGA 7892

QY 325 ----- 325
Db 7893 AAATGATTTTGAGGCACCTTTTGATGATTTTCAACTGATCAATTTGAATCAATTTGATGCCCA 7952
QY 326 -----Arg----- 326
Db 7953 AGATGATATAAAATTTCTAAAGTCACCTTCGGTCTATATAATCCATCAGTGGCGCTATGT 8012
QY 327 -Ala-----Gly-----Cys-----Val 330
Db 8013 AAGCATTTGAAAATTTTGAACATGCTACGTACTTACAAAAAGTATCCCTTCAGCTGAAGT 8072
QY 330 1-----Tyr----- 331
Db 8073 GGAGAAATGACACAATCATCATCTGCTGATTTCTTGAAGAAAAATACACTTAAAGA 8132
QY 332 -LeuLeu-----Pro-----Le 335
Db 8133 ACTATATGAGGTGATTTGGTTGTGCTGCTGATGATCTTTGAGGTATATTTGAAACACCT 8192
QY 335 uLeu-----Val-----Leu-----HisLeu-----LeuLeu 343
Db 8193 CTTACCAAAATTTGAAAAATCTCTTTATGATGCAAAATTTAGACACTTGTATCTACCTTAA 8252
QY 343 8-----Phe 344
Db 8253 GAATAGATTTCAAGTGTCTGAGGAATATCAGAGATTAGGAACAACCTTTT 8304

RESULT 13
LOCUS
AK090134
DEFINITION
Mus musculus 7 days embryo multipotent stem cell CRJ-2070 NE cDNA,
RIKEN full-length enriched library, clone:G431003J08
product:meiotic check point regulator, full insert sequence.

ACCESSION
VERSION
AK090134.1 GI:26105747
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
3 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
4
5 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
6
7 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection

```

JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
          Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
JOURNAL of 60,770 full-length cDNAs
REFERENCE Nature 420, 563-573 (2002)
AUTHORS 6 (bases 1 to 8928)
          Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
          Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
          Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
          Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
          Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
          Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
          Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
          Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
          Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
          Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
          Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
          Muramatsu,M. and Hayashizaki,Y.
          Direct Submission
TITLE Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
JOURNAL Physical and Chemical Research (RIKEN), Laboratory for Genome
          Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
          RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
          Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
          URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
          Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
          Encyclopedia Project of Genome Exploration Research Group in Riken
          Genomic Sciences Center and Genome Science Laboratory in RIKEN.
          Division of Experimental Animal Research in Riken contributed to
          prepare mouse tissues.
          Please visit our web site for further details.
          URL:http://genome.gsc.riken.go.jp/
          URL:http://phantom.gsc.riken.go.jp/.
FEATURES
source
    1. .8928
        /organism="Mus musculus"
        /mol_type="mRNA"
        /strain="C3H/J"
        /db_xref="FANTOM DB:G431003J08"
        /db_xref="MGI:2429040"
        /db_xref="taxon:10090"
        /clone="G431003J08"
        /cell_line="CRU-2070 NE"
        /cell_type="nullipotent stem cell"
        /clone_lib="RIKEN full-length enriched mouse cDNA library"
        /dev_stage="7 days embryo"
        251..6084
        /notes="meiotic check point regulator (MGD|MGI:103097,
        GB|NM_008569, evidence: BLASTN, 99%, match=6325)
        putative"
        8910..8915
        /note="putative"
        8928
        /note="putative"
misc_feature
    251..6084
        /notes="meiotic check point regulator (MGD|MGI:103097,
        GB|NM_008569, evidence: BLASTN, 99%, match=6325)
        putative"
polyA_signal
    8910..8915
        /note="putative"
polyA_site
    8928
        /note="putative"
ORIGIN
Alignment Scores:
Pred. No.: 2,54e-13 Length: 8928
Score: 1691.80 Matches: 287
Percent Similarity: 11.94% Conservative: 44
Best Local Similarity: 10.35% Mismatches: 9
Query Match: 70.26% Indels: 2432
DB: 11 Gaps: 248
US-10-017-084a-523 (1-344) x AK090134 (1-8928)
QY 1 Met-----1
Db 16 ATGGCTCCAGCCATTGAGTTTTCGCAAGTCTTTGGTGTCCCGTGCCTGCCGCCATTCCTTC 75

```

Db	1156	AGCACATCTCAGAAAGCCTCTCTCCAAAGCGGAATCCCTGTGGCTTCGCGGTTCAGAAATTA	1215
Qy	51	-----GluSer-----Ala-----Thr-----	54
Db	1216	CTCTTCATTACAGACCAGAGTCGCTCAACCTCTCTCGCCAGTCTACACTCTCGGTGCGC	1275
Qy	55	-----LeuArgCys-----	57
Db	1276	TTCCATTTCCAAACATGGCGGCTCTAAGTCGTGCTCACTCTCTCGCTTAGTGTGCACTC	1335
Qy	58	-----Thr-----	58
Db	1336	TTTCTCAGGGCGCAAGATTCACACTTTCAAGCCACAGTCAGTCACCAAGACACAGAC	1395
Qy	59	-----Ile-----AspAsnArg-----	62
Db	1396	CATTCTCACTCTCCGAGTGCAGTTTCAACGACTCATTTTGGCACACAGAAACAGAGCC	1455
Qy	63	-----Val-----Thr-----Arg	65
Db	1456	AATGTTCCTGAGCTGTGCATTGATCACTTATGGACTGAGACACTTCGGAATATAGAGA	1515
Qy	65	-----	65
Db	1516	GAATAATTCTCAAGCCTCCAAGGTATTTATAACGACTGACTGTGTGGACAGAAAGTTCTT	1575
Qy	66	-----Val-----	66
Db	1576	GTGCTTTTATGTGGAGGCCAGCTTCAGTTACGCTGTGTAAAGTTTCAAGAGAGTAATGA	1635
Qy	67	-----Ala-----TrpLeu-----Asn-----ArgSer-----	72
Db	1636	CAAGACTCAGCTTATCTTTGGCTCTGTCCACCAACATACATGCAAAAGACGACGCCAGTG	1695
Qy	73	-----Thr-----IleLeuTyrAlaGly	78
Db	1696	GGGAAGATACACACCATGTCTGTCTAGAAAGCAACGGGAACCTGGTGTCTGTACACAGGA	1755
Qy	78	-----	78
Db	1756	GTGTGCGGGTGGGAAAGTCTTTATCCCTGGACTTCGGGCTCTTCCCTGACAAATGTC	1815
Qy	79	Asn-----	79
Db	1816	AACATGATGCTCGGCGCAGTACCCCGCTCGACGGTGTGTGTACTCCAAGCCCTCTGAGT	1875
Qy	80	-----Asp	80
Db	1876	AAATTGCTTGGATCGATGGATGAGGTGGTCTGTGTCTCCAGTTCAGAAATTCAGGGAT	1935
Qy	81	-----Lys-----Trp-----Cys-----Leu-----	84
Db	1936	TCTTCAAAACCTTAATGATTCCTCTCAAAATGAGGATTCGATTCAGAGCAGCTTGGAACT	1995
Qy	85	-----AspPro-----ArgValValLeu-----LeuSerAsn-----	93
Db	1996	TACATTCACTGTGCGAGACCCCTGTTCAAAACAGATCACTCTAGAACTGAGCAATGGC	2055
Qy	94	-----Thr-----GlnThr-----	96
Db	2056	TCCATGGTTTCGATCACTATCCCTCAAGTGGCCACCTCGGAATTAGTACAAACGTGTCTG	2115
Qy	97	Gln-----TyrSerIle-----Glu-----IleGln-----	103
Db	2116	CAAGCAATTAAGTTC---ATCTGCGAAAGAGTAGCCATTTCAGGTGCTCGTCAAGTGG	2172
Qy	104	-----AsnVal-----	105
Db	2173	TACAAATGTGCAGTGTCCAGGAGGCCAGCTGTCTACTCAGAGTGGAGTTTATTTGTG	2232
Qy	106	-----ValTyr-----	108

```

QY 154 ---Ser---LeuThr-----156
Db 3373 CAAGTGCACAGCCTGTCGCGTCAATGTGTGTCAGTACCCAGAACTCAGTACGACCATGAG 3432
QY 157 ---Cys---IleAla-----159
Db 3433 TTCAATTGAAGAAAGAAACAGACTGCTCCAGTTGTGTGTCAGGAACTATGGCCCTTCCA 3492
QY 160 ThrGlyArg-----Pro---GluPro-----165
Db 3493 GTAGGACGAGGAGTGTATTACCTTGTCTCATATCACCTGTTCCACAGAGCGGTGCT 3552
QY 166 ---ThrVal-----167
Db 3553 GTTCCTAAATTGATCTGACAGGGGAGCCCTCCACGAAACACAACTGTATGATCTTAAT 3612
QY 168 ---ThrTrp-----ArgHis-----171
Db 3613 AGCGAAACATCGACGTGCTCCCAACATGGCCAGCTGGGCCAGCTTTCATATGGTGTG 3672
QY 172 ---Ile---Ser-----173
Db 3673 GTGCGGCGCTGAAGATAGCCCGAGCTCCAGATAGACTCAGCTTGGATCGTTTACAAC 3732
QY 174 ---ProLys-----Ala---ValGlyPhe-----179
Db 3733 AAGCCAAAGCNTGCTGAGTTAGCAATGAGTATGCGCGCTTCTCATGCGCCCTGGGTCTG 3792
QY 179 -----179
Db 3793 AATGGCACCTTACCAAGCTGGCTACTCTCAATATCCATGACTATTGTGACCAAGGCCAT 3852
QY 180 ---ValSer-----181
Db 3853 GAAATGACAAGCATTGGATTGTACTTGTGTGTTCTGCTGCAAGCTTGGCACCATTGGAC 3912
QY 181 -----181
Db 3913 ATGTCAATTACCGGCTCCTCAGCATTCAGTTCCTGCTCTCTTACCCCGCATCCACA 3972
QY 182 Glu---Asp-----183
Db 3973 GAGCTTGAGTGCGCTCACAATGTCCAAGTGGGGCTGTGTTGGCATTTGGCCCTTGTGTAT 4032
QY 183 -----183
Db 4033 CAGGGCACAGCTCAGACACACTGCGGAAGTCTGTGCTGGAATAGGGCGGCCCT 4092
QY 184 ---GluTyrLeu-----Glu-----187
Db 4093 GGTCCGGAATGGAATACTGCACTGACAGAGTCTACTCTCTAGCTGCTGGCCCTGGCC 4152
QY 188 ---Ile-----188
Db 4153 CTGGGATGTTTGTGTGGGATGCGCAATTTGATTGGCATGTCTGATCTCAATGTG 4212
QY 189 ---Gln-----Gly-----Ile---Thr-----192
Db 4213 CTTGACAGCTGTATCAGTACATGTTGGAGGCCATAGGCGATTTCAAACCTGGAATGCAC 4272
QY 193 ArgGlu-----Gln-----195
Db 4273 AGGAGAAACATAAGTCTCCAAGTTATCAGATCAAAAGAGGAGACACCATAAAGCTGGAT 4332
QY 196 ---Ser---Gly-----197
Db 4333 GTGACTGTGCCGGTCTACTCTGGGCTGGCTATGATGATCTACTTAAAAACCAATACAGG 4392
QY 198 ---Asp-----Tyr-----199
Db 4393 TCCATTGCTGATTGGTGGTGGTCTGCTGATACCATGATATTGTGTAGACTTTGTGAACCA 4452

```

```

QY 200 Glu-----Cys-----201
Db 4453 GAATTCCTTTTCTTAGGACACTTGTCTGGTCTGATTTTGTGGATGATATCTTTACCA 4512
QY 202 ---Ser---AlaSerAsn-----205
Db 4513 AATTCCAAGTGGTGTGACGACCAATGTTCTCAGATTATAAGAGAAAATAGTATCTCTCTG 4572
QY 206 ---Asp-----206
Db 4573 AGTGAATTTGAATTGCTTGTTCAGAGGACTTGAATTTGGAACCTTGTGCAAGCACAC 4632
QY 207 Val-----207
Db 4633 GTCTACATCAITGACAGGAGCCTGTGCTCTAGGGTTTCGATTTGCTGGCTCAGAAAC 4692
QY 208 ---Ala-----Ala-----209
Db 4693 TTATCAGCATTTAGCTGTCTGCATAAATTTGCAAAAGATTTTATGAATTTATTTCTGCA 4752
QY 210 Pro-----ValVal-----212
Db 4753 CCCAATGCTTCTGTAAACAGGGCCCTATAACCTCGAAACCTGCTGAGTGTGCTCTGCTG 4812
QY 212 -----212
Db 4813 TCTCTGCCATGGTGTATGGCTGCTGGAACCTGAAGGTGTTCAGCTGTGTCGCTTT 4872
QY 212 -----212
Db 4873 CTGCACATGAAGACTGCTGAGAGATGAATATGCTTCCACTTGGCCACCACCATGGCC 4932
QY 212 -----212
Db 4933 CTGGCCCTTCTCTTTTGGAGGAGAAAGTACTCTTTTTCAGCATCCAACTCATCCATT 4992
QY 212 -----212
Db 4993 GCTGCCCTTCTGTGCGCTTTTACCACATTTCCCGCCACAGCAGCTGACAAACCGGTAT 5052
QY 213 ---Arg---ValLys-----ValLys-----216
Db 5053 CATCTCCAGGCCCTTGGCACCTCTATGTGTAGCTGCGAAGCAAGGCTCTCTGCTACT 5112
QY 217 ValThrVal-----Asn-----220
Db 5113 GTAGATGTGATPACAAACACACACCCCTGCTATGCCCTTATAGAGTTACTTACAAGGCACT 5172
QY 221 ---Tyr-----Pro-----222
Db 5173 CAGTGGTATGAACAGACCAAGAGAACTGATGGCTCCACCCCTTCTCCAGAACTTCAT 5232
QY 223 ---Pro---Tyr-----Ile-----Ser-----226
Db 5233 CTTTAAAGCAGATGAAAGTTAAAGGGCCAAAGTACTGGGAACCTCTCATAGATTTAAGC 5292
QY 227 ---Glu-----AlaLys-----229
Db 5293 AAGGAGAACACGACTTGGAGTCTATTTCTTCCAAAGGATGGAGTTTATATGTAAGCTC 5352
QY 230 ---Gly---Thr-----Gly-----232
Db 5353 AGGGCAGGACAGCTCTCTCTACAAAGAACCCAACTGGGTGGCAGAGTTTGTGGCAACNA 5412
QY 233 ---Val-----233
Db 5413 ACTGTGGCAATAGGAACCTGAGCCCGGCTTCAAGCCCTGAAACAAATTCATCATTC 5472
QY 234 -----Pro---Val-----235
Db 5473 ACTTCTGATCCAGCACTTCTGTCTATTGCTGAATATTTCTGCAAGCCGACTGTGAGCATG 5532
QY 236 Gly-----236

```



```
QY 319 -----Val-----Ser-----AsnGly-----Thr---Ser--- 324
Db 7744 GCTTTGAGTGTAGTACTGTCAGCAGACAGACATGGAGCGGTGTGCTCAGATCTTTC 7803
QY 325 -----Arg-----Arg----- 326
Db 7804 CCAAAGGCTACTGACGCTGTCTCTTCTCCTCTTGGTCTAACGTTGGAGGTGAAGGAAA 7863
QY 326 ----- 326
Db 7864 CTGAGCTCAGATGCCAAACTTCAACTACTACTCATCATATGTTCTCAACATCCTGGAC 7923
QY 326 ----- 326
Db 7924 TCTACCTATCTGCTACACCCAGCCCTGCTGTGCTGTGCTGCTGCTGATGATTCGA 7983
QY 326 ----- 326
Db 7984 GTCCAAGAGAAATCAGAAACAACCTCAATGTGAACGTGAAGGCTCTTAGCGTTGGCAGAGCTT 8043
QY 327 -----Ala-----Gly---CysVal----- 330
Db 8044 CTGAACATGTTGAAGCAGCAGCAACCTTGCATCAGATGGGCTTTTGTGTGTTTCT 8103
QY 331 -----Trp----- 331
Db 8104 TGATGTTCTCCCAATTGACTTAGTCATCATCTATTGGTCACATATATAGAGCATCTGTT 8163
QY 332 ----- 332
Db 8164 TAAGCTTTTGTCTTTTAGCTAAAAACACTTCTTTGGTAAACCTTTTAAATGCAATCTT 8223
QY 333 LeuProLeu---Leu---ValLeu-----LysPhe 344
Db 8224 TTTCCTTTAGATATTTTGGAGTGACTTTTAAAGCTTTTCTTCTTGAACATTCAT 8283
QY 340 -----LeuLeu-----LysPhe 344
Db 8284 ATCAGAAATTTAAACACGGAACCTTCATAATAAATTT 8319

RESULT 14
LOCUS AY404418
DEFINITION Homo sapiens LRP1 gene, VIRTUAL TRANSCRIPT, partial sequence,
ACCESSION AY404418
VERSION AY404418.1 GI:39760395
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 12485)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 12485)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment
FEATURES Location/Qualifiers
```

```
source 1..12485
/morganism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>12485
/gene="LRP1"
/locus_tag="HQM1884"

gene
ORIGIN
Alignment Scores: 1.36e-12 Length: 12485
Pred. No.: 1688.70 Matches: 294
Score: 10.52% Conservative: 40
Percent Similarity: 9.26% Mismatches: 7
Best Local Similarity: 70.13% Indels: 2833
Query Match: 29 Gaps: 262
DB:
US-10-017-084A-523 (1-344) x AY404418 (1-12485)
QY 1 Met-----LysThrIle----- 4
Db 630 ATGGACTTCAGCTATGCCAACGAGACCGTATGCTGGGTGCATGTTGGGACAGTGTCT 689
QY 5 -----Gln-----Pro-----Lys-----Methis--- 9
Db 690 CAGACGCAGCTCAGTGTGCCGCGATGCTGCTAAAGGGCTTCGTGGATGAGCACACC 749
QY 10 ---Asn-----Ser-----Lys-----IleSerTrp----- 14
Db 750 ATCAACATCTCCCTCAGTCTGCACACGTCGACAGATGGCCATCGACTGGCTGACAGC 809
QY 15 -----Ala-----IlePhe----- 17
Db 810 AACTTCTACTTTGTGGATGACATGATGATAGTATCTTTGTCTGCAACAGAAATGGGAC 869
QY 18 -----Thr-----GlyLeuAla----- 21
Db 870 ACATGTGTACATTTCTAGACCTGGAACTCTACAAACCCCAAGGCGATTTGCCCTGAC 929
QY 22 Ala-----Leu-----Cys--- 24
Db 930 GCCATGGGGAAGGTGTTTTTCACTACTATGGGAGATCCCAAGGTGAACGCTGTGAC 989
QY 25 -----Leu-----Phe----- 26
Db 990 ATGGATGGCAGACCGCAGCAAGCTCTCGACAGCAAGATTGTCTTCTCATGGCATC 1049
QY 26 ----- 26
Db 1050 ACGCTGGACCTGGTCAGCCGCTTGTCTACTGGGAGATGCTATCTGGACTATATTGAA 1109
QY 27 -----GlnGly----- 28
Db 1110 GTGGTGGACTATAGGGCAAGGCCCGCAGACCATCATCCAGGGCATCTTGATTGACAC 1169
QY 28 ----- 28
Db 1170 CTGTACGGCTGACTGTGTTTGAGAATTATCTCTATGCCACCAACTCGGCAATGCCA 1229
QY 28 ----- 28
Db 1230 GCCCAGCAGACAGACGAGTGTGATCCGTGTGAACCGCTTTAAACGACCGAGTACAGG 1289
QY 29 -----Val-----Pro--- 30
Db 1290 GTCAACCGGGTGGACAGGGTGGTGGTCCCTCCACATCTACCACGAGGGCGTCAGCC 1349
QY 31 ValArgSer-----Gly-----Asp--- 35
Db 1350 GTGAGGAGCCATGCTGTGTGAAAACGACCATGATGGAGCCGGTGGTGTCTCTGAC 1409
QY 36 -----Ala---Thr-----Phe----- 38
```


Db 1410 TGCCTGCTGGCCAAACAGCCACGAGCGCGACCTGCGCTGCGCTTCGGGCTTCAGCGCTG 1469
QY 39 -----Pro-----Lys 40
Db 1470 GGCAGTGACGGGAAGTATGCAAGAAGCCGAGCATGAGCTGTTCTCGTGTATGGCAAG 1529
QY 41 -----AlaMetAsp----- 43
Db 1530 GGCAGCGCAGCATCATCCGGGGCATGGATATGGGGCCCAAGGTCCCGGATGACACATG 1589
QY 44 -----Asn----- 44
Db 1590 ATCCCAATTGAACCTCATGAACCCCGAGCCCTGGACTTCCAGCTGAGACGGGCTTC 1649
QY 45 Val-----Thr-----Val-----ArgGln-----Gly----- 50
Db 1650 ATCTACTTTGGCAGACACCAACAGTACTCATTTGGCGCCAGAAAGATTGATGGCACTGAG 1709
QY 51 --GluSer-----Ala----- 53
Db 1710 CGGGAGACCATCTGAAGGACGGCATCCACAATGTGGAGGGTGTGGCGTGGACTGGATG 1769
QY 54 -----Thr-----Leu 55
Db 1770 GGAGACAATCTGTACTGACGCGACGATGGGCCCCAAAAGACAATCAGCGTGGCCAGGCTG 1829
QY 56 -----Arg-----Cys-----Thr----- 58
Db 1830 GAGAAAGTGTCTAGACCCCGCAAGACTTTAATCGAGGGCAAAATGACACCCCGAGGCT 1889
QY 59 Ile-----Asp-----Asn----- 61
Db 1890 ATTGTGTGGATCCACTCAATGGTGGATGACTGGACAGACTGGAGAGGAGCCCAAG 1949
QY 62 -----Arg----- 62
Db 1950 GACAGTGGCGTGGCGCGCTGGAGAGCGCTGGATGGATGCTCACACCGAGACATCTTT 2009
QY 63 ValThr--Arg--Val-----Ala----- 67
Db 2010 GTCACCTCAAGACAGTGTCTTTGGCCCAATGGGCTAAGCCTGGACATCCCGCTGGGGCG 2069
QY 68 -----Trp----- 68
Db 2070 CTCTACTGGGTGGATGCTTCTACGACCGCATCGAGAGATGCTCTCAATGGCAGAC 2129
QY 69 -----LeuAsn----- 70
Db 2130 CGGAAGATTGTATGAAGGCTCTGAGCTGAACACACGCTTTTGGCTGTGTCAACATGGC 2189
QY 71 -----ArgSer----- 72
Db 2190 AACTACCTTCTTGACTGAGTATCGAGTGGCAGTGTCTACCGTTTGGAAAGGGGTCTA 2249
QY 73 -----Thr-----Ile 74
Db 2250 GGAGCGCACCCCACTGTGACCTTCTGGCAGTGAAGCGGCCCCCATCTTTGAGATC 2309
QY 75 --LeuTyr--Ala-----Gly-----Asn-- 79
Db 2310 CGAATGATATGATCCAGCAGAGCAAGTTGGCACCAACAATGCGCGGTGAACAATGGC 2369
QY 79 ----- 79
Db 2370 GSGTCAGCAGCTGTGTGGCCACCCTTGGGAGCCCGCAGTGGCGCTGTGCTGAGGAC 2429
QY 80 -----Asp----- 80
Db 2430 CAGGTGTTGGAGCAGAGCGGTCTACTTGTGGCGAAACCCATCTTACGTGCTCCACCC 2489
QY 81 ----- 82
Db 2490 CAGTCCAGCCAGGCGAGTTTGCCTGTGCGCAACAGCCGCTGCATCCAGGAGCGCTGGAA 2549

QY 83 -----CysLeuAsp----- 85
Db 2550 TGTGACGAGACAACGATTGCTGGACAACAGTGTAGGCCCCAGCCCTCTGCCATCAG 2609
QY 86 -----Pro-----ArgVal-----Val----- 89
Db 2610 CACACCTGCCCCTCGGACCGATTCAAGTGGGAGAACACCGGTGCATCCCCCAACCGCTGG 2669
QY 90 LeuLeu-----SerAsn-----Thr----- 94
Db 2670 CTCTCGACGGGACAAATGACTGTGGGAACAGTGAAGATGAGTCCAATGCCACTTGTTC 2729
QY 95 --GlnThr--GlnTyrSer-----IleGluIle-- 102
Db 2730 GCGCGACCTGCCCCCACCAGTTCTCTGTGCCAGTGGCGCTGCATCCCCATCTCC 2789
QY 102 ----- 102
Db 2790 TGGACGTGTGATCTGGATGACGACTGTGGGACCGCTCTGTATGAGTCTGCTTCTGTGCC 2849
QY 103 -----Gln-----AsnVal 105
Db 2850 TATCCCACTGCTTCCCGCTGACTCAGTTTACCTGCAACAATGGCAGATGATCAACATC 2909
QY 106 -----Asp----- 106
Db 2910 AACTGGAGATGCGACAATGAATGACTGTGGGGACAACAGTGACGAGCGGCTGCAGC 2969
QY 107 -----Val----- 107
Db 2970 CACTCTGTTCTAGCACCCAGTTCAAGTGCACAGCGGGGTTGTCATCCCCGAGACTGG 3029
QY 108 -----Tyr----- 108
Db 3030 ACTGCGATGGGACAATGACTCGGAGACTACAGTGATGAGACACACGCAACTGCACC 3089
QY 109 -----AspGlu----- 110
Db 3090 AACCAGGCCACGAGGCCCTTGGTGGCTGCCACACTGATGAGTTCAGTCCCGCTGGAT 3149
QY 111 Gly-----Pro-----Tyr----- 113
Db 3150 GGACTATGATCCCGCTGGCTGGCGTGGCGTGGAGGACACTGACTGCATGACTCCAGC 3209
QY 114 -----Thr-----Cys-----SerVal----- 117
Db 3210 GATGAGAAGAGCTGTGAGGAGTGACCCACGCTTCGATCCCGATGTCAGTTTGGCTGC 3269
QY 118 -----Gln----- 118
Db 3270 AAGGACTCAGTCGGTGCATCAGCAAGCGTGGGTGTGTGATGGCGACATGACTGTGAG 3329
QY 119 -----ThrAsp-----Asn-----HisPro-- 123
Db 3330 GATAACTCGGACGAGGAGAACTGCGAGTCCCTGGCTGCGAGGCCACCGCTGCACCTTGT 3389
QY 124 -----LysThrSerArgVal----- 128
Db 3390 GCCAACAACCTCA---GTCGTGCTGCCCTGACAGCTGTGTGATGGCAAGCAGCAC 3446
QY 128 ----- 128
Db 3447 TGTGGCGACGCTCAGATGAGGGCGAGCTCTGCGACCGAGTGTCTCTGAATAACGTTGCC 3506
QY 129 -----His-----Leu-----IleVal----- 132
Db 3507 TGCAGCCACAACACTGCTCAGTGGCAGCTGGCGAAGGCAATGTGTGTTCTCCCTCTGGGC 3566
QY 132 ----- 132
Db 3567 ATGAGCTGGGGCCGCAACCAACCTGCCAGATCCAGAGTACTGTGTCGAAGCATCTC 3626

QY 133 -----Gln----- 133
Db 3627 AAATGAGCAAAAGTGGACCAAGAACAAAGTTACAGGTGAAGTGTCTGTGTACAGGGC 3686
QY 134 ---Val-----Ser-----Pro---Lys-----Ile 138
Db 3687 TGGGTCTCTGGAACCTGACGGCGAGAGCTGTGCGAGCCTGGACCCCTTCAAGCGCTTCATC 3746
QY 139 Val-----Glutile----- 141
Db 3747 ATTTTCTCAACCGGCATGAATCCGGCGCATGATCTTCAAAAGGAGACTACAGCGTC 3806
QY 142 -----Ser-----Ser----- 143
Db 3807 CTGGTCCCGGCTGCGCAACACCATCGCCCTGGACTTCCACCTCAGCGAGAGCCCTC 3866
QY 144 -----Aspile-----Serile-----Asn----- 148
Db 3867 TACTGGACCGAGTGTGGAGGACAAGATCTACCGGGGAAGTGTGTGACAAACGAGCC 3926
QY 149 -----Glu----- 149
Db 3927 CTGACTAGTTTCGAGTGGTGAATCAGTATGSCCTGGCCACACCCGAGGGCCTGCTGTGA 3986
QY 150 -----GlyAsn-----Asn-----Ile----- 153
Db 3987 GACTGGATTGACAGGCAACATCTACTCTGGTGGAGAGTAACTTGGATCAGATCGAGTGGCC 4046
QY 154 -----Serleu-----Thr-----Cys----- 157
Db 4047 AAGCTGGATGGAGACCTCCGGACCACTCTGGCCGCTGACATTTGAGCAACCAAGGCA 4106
QY 158 IleAla-----Thr----- 160
Db 4107 ATCGCACTGGATCCCGGATGGATCTCTGTTTGGACAGACTGGGATGCCAGCTGGCC 4166
QY 161 -----GlyArg----- 162
Db 4167 CGCAATTGAGGACGCTTCATGATGGGCTGGCGCGCCGACCGTGCACGGGAGACCGGC 4226
QY 163 -----Pro----- 163
Db 4227 TCTGGGGGTGGCCCAACGGGCTCACCGTGAACCTGAGACTACCTGGAGAGCGCATCTTTGGATT 4286
QY 163 -----Glu-----Thr-----Val 167
Db 4287 GACGCCAGTCAAGTCCATTTACTCAGCCCGTTAGACGGCTCTGGCCACATGAGGGTG 4346
QY 164 -----Glu-----Pro-----Thr----- 167
Db 4347 CTTCGGGGACAGAGTTCCTGTGCGACCCGTTTGCAGTGACGCTGTACGGGGGGAGGTG 4406
QY 168 -----Thr---TipArg----- 170
Db 4407 TACTGCACTGACTGGCGAACAACACACTGGCTAAGGCCCAAGTGGACCGGCCACAAAT 4466
QY 170 ----- 170
Db 4467 GTCAACGTTGACAGAGGACCAACACCCAGCCCTTTGACCTGCGAGTGTACCAACCCCTCC 4526
QY 171 -----His 171
Db 4527 CGCCAGCCCATGGCTCCCAATCCCTGTGAGGCCAATGGGGGCGCGAGCCCTGCTCCCAAC 4586
QY 172 -----Ile-----Ser-----Pro----- 174
Db 4587 CTGTGCTCATCAACTAACAACGAGCCGTGTCTGCGCCCTGCCCCACCTCATGAGGTG 4646
QY 175 -----Lys-----Ala----- 176
Db 4647 CACAAGGACAACACCCCTGCTATGAGTTTAAGAGTTCCTGTGTACGCAAGTCAAGT 4706
QY 177 ---Val---Gly-----Phe----- 179

Db 4707 GAGATCCAGGTGTGGACCTGGATGCTCTCCCTACTACAATACATCATCTCTTACGGTG 4766
QY 180 -----ValSer-----Glu----- 182
Db 4767 CCCGACATCGAACACGTCAACAGTGTAGACTACGATGCCCGGAGCAGCGTGTGTACTGG 4826
QY 183 ---Asp-----Glu----- 184
Db 4827 TCTGACGTGCGGACACAGGCCATCAAGGGGCTTTCATCAACGGCACAGGCGTGAGACA 4886
QY 184 ----- 184
Db 4887 GTGCTCTCTCGAGACTTGCCTCAATGCCCCACGGGCTGGCTGTGGACTGGGTCTCCCGAACA 4946
QY 185 -----Tyr----- 185
Db 4947 CTGTTCTGGCAAGCTATGACCAATTAAGAGCAGATCAATGTGGCCCGGCTGGATGGC 5006
QY 186 -----LeuGlu----- 187
Db 5007 TCCTTCAAGAACGAGTGTGTCAGGGCTGGAGAGCCCCATGGCTTGTCTCCACCGT 5066
QY 188 -----Ile----- 188
Db 5067 CTGCTGGGAAAGCTCTACTGGACCGATGGTGACACATCAGCATGGCCCAACATGATGGC 5126
QY 189 -----Gln-----Gly----- 190
Db 5127 AGCAATCGACCCCTCTCTTCAAGTGGCCAGAGGGCCCGCTGGGCTTGTATTGACTTC 5186
QY 191 -----Ile-----Thr-----Arg----- 193
Db 5187 CCTGAAAGCAAACTCTACTGGATCAGTCTCGGGAACCATATCAATCAACCGTGCACCTG 5246
QY 194 -----Glu-----Gln-----Ser----- 196
Db 5247 GATGGAGTGGCTGGAGGTTCATCGATGCCATGGAGGACGATGGGCAAGCCACCGC 5306
QY 197 -----GlyAsp-----Tyr-----Glu----- 200
Db 5307 CTGGCCATCATGGGGGACAAAGTGTGTGGGCTGATCAGGTGTTCGAAAGATGGGCACA 5366
QY 201 CysSer---Ala-----Ser-----Asn----- 205
Db 5367 TGCAGCAAGGCTGACGGCTCGGGCTCCGTGGTCTTTCGGAACAGCACACCCTGGTGATG 5426
QY 206 -----Asp----- 206
Db 5427 CACATGAAGGTCTATGACGAGAGCATCCAGTGGACCATTAAGGGCACCAACCCCTGCAGT 5486
QY 207 Val----- 207
Db 5487 GTCAACAAAGGTGACTGTCTCCAGCTGTGCTGCCCTGTGCCACGTTCAGAACGCCGTCTGC 5546
QY 208 -----Ala----- 208
Db 5547 ATGTGCACAGCGGCTATAGCTCCGGAGTGGCCAGCAGGCTTCGAGGGCGTAGGTTC 5606
QY 208 ----- 208
Db 5607 TTTCTCTGTACTCTGTGATGAGGGAATCAGGGGAATTCCTCTGGATCCCAATGACAAG 5666
QY 209 -----Ala-----ProVal-----Val----- 212
Db 5667 TCAGATGCCCTGTGCTCCAGTGTCCGGGACCTCGCTGGCTGTGGCATCGATTCACCGCT 5726
QY 212 ----- 212
Db 5727 GAAATGACACCATCTACTGGGTGGACATGGGCTGTGAGCAGATCAGCCCGCCCAAGGG 5786
QY 213 -----Arg-----ArgValLys----- 216

[illegible]


```
QY 10 -----Asn-----Ser----- 11
Db 3958 CACTTTTCAATCCCAAGACACATCAGCTGCAAGTGCCCTCTCTTTGGGCAATTCGGAACCT 4017
QY 12 -----IleSer-----Trp----- 14
Db 4018 TTCCACAAATGCTACAGCAACTTGTACAACTGGTCACTCTCTACACCTGGTGGCAACAC 4077
QY 14 ----- 14
Db 4078 CAGCAGGATCACTTCAGCGCTTCAGGCTCAGTACCGCATGAAGGCTGACTCTGTGGTTGA 4137
QY 15 -----Ala-----Ile 16
Db 4138 CTGTGTTTCCTACAGTGTGAAGGATCTGGAGAAACAACATAGCAGCAAGAGCACATT 4197
QY 17 -----Phe-----Thr----- 18
Db 4198 CACTTTATCGTGTGATGGGTCTCTACATCAATAATTTCTAGATTCCAAATTCAAAGTCAG 4257
QY 18 ----- 18
Db 4258 CCACGTAGAAATTTGGAACAACCCAGTCTCGAAAGGTTTATTAACATTTGAAACATC 4317
QY 19 -----Gly-----Leu-----AlaAlaLeu----- 23
Db 4318 TAGTGCCTTGGGACCACAGATGCTGCTACAGTTCACTGAGTGGACTCAAAAAGAAACAACA 4377
QY 24 -----Cys----- 24
Db 4378 TCTGTATGTCAAAGACATCAAGGTTGACGGACAGTTCAGAGTATTTTCATTGTACGCTCA 4437
QY 25 -----Leu-----Phe----- 26
Db 4438 AGTGAATATGCGCTGTCTTATGAGAGAGATTCTATGACTGCCAGATGAGCGGAGAAATC 4497
QY 27 -----Gln-----Gly---ValPro 30
Db 4498 CAACATGAAATTAATCCACCTACTTCCAGGGCACCACACAGATAGTGGGAAATGTACCA 4557
QY 31 -----Val-----Arg----- 32
Db 4558 GGATGGAATGCTGTGTCTCACTTCCACCTCTGACCTGCAAGATGGCAATATTCAGAAACAC 4617
QY 33 -----Ser----- 33
Db 4618 AGCTTCCCTAAATATGAAAACTATGAGTGTGACTCTGAAATCCGACAGCGTGGGCACTA 4677
QY 34 -----Gly---Asp----- 35
Db 4678 TGAGAACCTTTGCTGCTTCCCAACAGCTGGACATGACCTTCTTAACCAAGCGCACTGCT 4737
QY 36 Ala-----Thr----- 37
Db 4738 GCGTTCTGAACACCGGCAACTACAAGTCCCTGAGACTTGTCAACCTTCTTCTGGATC 4797
QY 38 -----PhePro-----Lys----- 40
Db 4798 CCTCACTTCCAGGGGTAGAAATTAATGCTGACATCTTTGGGACCGACAAATTAATAC 4857
QY 41 -----AlaMetAsp----- 44
Db 4858 TGGTGTCTCAAGTCAACGCTAAGATTGCACAAGATGGAGTATCTACAGTGCACACCAC 4917
QY 45 -----Val-----Thr-----Val---ArgGln----- 49
Db 4918 CAACTTAAAGTACAGCCCGTCTGCTGTGAGAAATGAGTTGAACGCGACAGCTTGGGCTCTC 4977
QY 50 -----Gly----- 50
Db 4978 TGGGGCATCCATGAATTTGTCAACAAGTGGCGCTTCAAAGAAACACCATGCAAAATTCAG 5037
QY 51 -----GluSer-----AlaThr-----Leu----- 55
```

```
Db 5038 TCTTGATGGGAGAGCTGCCCTCAACAGAGGTATCACTGGGAAGCATTTTACCAGGCCCATGAT 5097
QY 56 -----Arg-----Cys-----Thr----- 58
Db 5098 TCTGGGTGCAGACAGCAAAAATGCTTCAAACTTCAAACTCAGCCGAGAGAGACTGAAGCT 5157
QY 59 Ile-----Asp-----Asn-----Arg----- 62
Db 5158 ATCCAATGACATGATGGGCTCTCTAGCTGAAATGAAACTCGACCAACACACACAGTCTGAG 5217
QY 62 ----- 62
Db 5218 AATTTCAAGTCTCTCCCTGGAGCTTCTTCTCAAAAATGGAACAATATTTACAGTGGAGACAA 5277
QY 63 Val-----Thr----- 64
Db 5278 GTTTTATAAGCAGAAATTTTAACTTACAGCTACAGCCCTATTCTTTTGGAAATTACTTTAAG 5337
QY 65 -----Arg-----Val----- 66
Db 5338 CAATGATCTGAAATATGATGCTCTAGTTTTCACCAACAATGGAAGTTTACGGCTGGAACC 5397
QY 67 -----Ala-----Trp---Leu---Asn----- 70
Db 5398 ACTGAACTGAAATGTTGGGTGGCAACTTTTAAGGGAACTTACCAAAATATATGAGCTGAACA 5457
QY 71 -----Ser-----Arg----- 72
Db 5458 CATCTATACCATCTCTTATAGTACCTGGTGTAGTAAAGTTTACAGAGCAGACACTGTAGC 5517
QY 73 -----Thr-----Ile----- 74
Db 5518 TACGGTTTCAGGGTGTGGAGTTTCAGCCATAGCTAAATGCAGACATCGAAGGCTGGCTTC 5577
QY 75 Leu-----Trp---Ala----- 77
Db 5578 CTCGGTTGATGCTCACTACCACTACAGTTTCAAGTCCACTGTCATTTTAACAATGTTTCCG 5637
QY 78 -----Gly-----Asn 79
Db 5638 CTTTGTCTGCGACCGTTTACCTTGGGCGTCGACACACATACAAAGTGTGTGAGGAAAT 5697
QY 79 ----- 79
Db 5698 GTCCCTCTGGGAGAAACACACTGGGCGAGTGTACAGTAAATTTCTGTTGAAAGCAGAAACC 5757
QY 79 ----- 79
Db 5758 TCTGGCACTTACCTTCTCTCATGACTACAAAGGATCCACGAGCCACATCTCCTGTACAA 5817
QY 79 ----- 79
Db 5818 GAACAGCGTCAGTACAGCTCTTGAGCACACACTCAGTGCCTTGTGACTCCAGCTGAACA 5877
QY 80 AspLys----- 81
Db 5878 GACAGCAGCTGGAAAATTCAGACCCAGCCTGATGACAAAGTATACAGCCAGGAATTTGA 5937
QY 82 -----Trp 82
Db 5938 AGCCTACAACACTAAAGACAAAATTTGGTATCGAGCTTAGTGGCGGCTGACCTCTCTGG 5997
QY 83 -----Cys----- 83
Db 5998 GCTGTACTCTCCAATTAAGTGGCGTTTTTCTACAGTGAGCGCTGTCAATGTCTTAAATAG 6057
QY 84 Leu---Asp-----ProArgVal----- 88
Db 6058 CTTGGAGATAAATGATGCTTTGAGAGCCCGAGAAATTCAAATTTGATGCTGTGGTGAA 6117
QY 89 -----ValLeu----- 90
```

Db 6118 ATACGATAGAACCAAGATGTCACACTATCAGCCTCCCATTTCTTCCAAAGCCTGCCAGA 6177
Qy 91 Leu-----Ser-----Asn-----Thr----- 94
Db 6178 TTAFTTGGAGAGAAATCGAAGAGGAAATTATAAGTCTACTGGAGCCATGAAGGGGAATT 6237
Qy 95 -----Gln-----Thr-----Gln----- 97
Db 6238 ACAACGCTCAGTGTGATCAGTTTGTGAGAAATATAGATGGCCCTGAGCAGGCTTCC 6297
Qy 98 -----TyrSer-----Ile-----Glu----- 101
Db 6298 TCACGAGATTCATGATTAATCTGAATGATCTGACTGGGAGAGACAAGTAGCTGGTGCAA 6357
Qy 102 -----Ile----- 102
Db 6358 GGAAATTAATTAATCTTTTCATGGAAACTATAGAAATTACAGATAATGATGACTAATTGC 6417
Qy 103 -----GlnAsn----- 104
Db 6418 CTTAGATAGTGCCAAATCAACTTTGAATGAAAACTCTCTCAACTTGAGACATACGGAT 6477
Qy 105 -----Val----- 105
Db 6478 ACAATTTGATCAGTATATTAGAGATAATTATGATGCACAGGACTTAAAAAGAACTATTGC 6537
Qy 106 -----Asp-----Val-----Tyr----- 108
Db 6538 TCAGATTATTGATAGAATCAATTGAAAGCTTAAAAAGCTTAAAGTCTTGACGACAGTATCATATCCG 6597
Qy 108 ----- 108
Db 6598 TGTAAATCTAGCAAAATCAATCCATAATCTCTATTATTATTGTTGAAAATGTTGATCTTAA 6657
Qy 109 -----Asp-----Glu----- 111
Db 6658 CCAATCAGTAGTAGTGTGGTCTTGATCCAAATGTGGATCCAAATATCAAAATCAG 6717
Qy 111 ----- 111
Db 6718 AATCCAGATACAGAAAACTCCAGCATCTCAGAACACAGATTCATAATATAGACATCA 6777
Qy 111 ----- 111
Db 6778 ACAGCTTGCTGCAGATTAAACACACAGATTGAAGCTCTTGATGCCAATGCATTAGA 6837
Qy 112 -----Pro----- 112
Db 6838 TCAACTGAGAACTGCAATTTCTATTCCAAAGAAATAAGTGTCAATTATTGAGCGTGTCAAATA 6897
Qy 112 ----- 112
Db 6898 CTTTGTATGAATCTTATTGAAGATTTTAAAGTAACCTGAGAAATCAATACTTTTAGAGT 6957
Qy 113 Tyr----- 113
Db 6958 TATAGTCGTGAGTTAAATTGAGAAATATGAAGTAGACCGCAAAATCCAGGTTTAAATGGA 7017
Qy 113 ----- 113
Db 7018 TAAATCAATAGATTGGCCCAAGATACAGCCTGAGTGAGCCTCTTCAGAAACTAAGTAA 7077
Qy 114 -----Thr----- 114
Db 7078 TGTGCTACGCAATTTGAGATAAAGACTACTATGATAAATGGTTGTTTATTATGATGA 7137
Qy 115 -----Cys-----SerVal-----Gln-----Thr----- 119
Db 7138 CACTGTCGAGTGAATTAAGCAGTGTCTTTCAAAAATATCATTAAGAACTGAATAGATT 7197
Qy 119 ----- 119
Db 7198 GATTGACATGTCGGTGAAAAAGTTGAAAGCCTTTGATTATATCACCAGTTTGTAGACAAAC 7257

Qy 120 -----Asp----- 120
Db 7258 CAACAGCAAAATCCGTGAGATGACTCAGAGAATCAATGCTGAAATCCAAGCTCTCGAACT 7317
Qy 121 -----AsnHis----- 122
Db 7318 CCACAGAAAACTGAAGCAATTAAACTGTGGGTAGAGACTTCAAAACCCACGGTCTCCAA 7377
Qy 123 Pro-----LysThr-----Ser-----Arg----- 127
Db 7378 CTCCTCGGAAAAAATCAAGAGCACCAAGTAATACTGTGGTCTGTGATTGGCTGCAGGATGG 7437
Qy 128 -----Val----- 128
Db 7438 TTTGGCTCAATAAAGCCCAATTTCCAAGATGCTTTAGAAGATGTACGAGACCGAAATTTA 7497
Qy 129 -----His-----LeuIleVal-----Gln 133
Db 7498 TCAATGGACATTCAGGGGAACTGGAGCGCTGCTGTCTCTGGTAAGCCAGTTTACAG 7557
Qy 134 -----Val-----Ser----- 135
Db 7558 CACAGTGTCACTACATTTCTGACTGTGTGGACTCTGACTGTCTAAAAAACAATACAGACTT 7617
Qy 136 -----ProLysIleVal-----Glu----- 140
Db 7618 TGCAGAGCAATATTCACCCAAAA-----GTGGGTGAGAGTGTGAAAGCACTGTGTGAACA 7674
Qy 141 Ile-----Ser-----Asp-----Ile----- 145
Db 7675 AGGATTCAITGTTCTCTGAAATCCAAACATTTCTGGGGACCATGCTGCAITTTGAGGTGAG 7734
Qy 145 ----- 145
Db 7735 TCTCCAGCTCTCCAAGAAGCTTAATTTTCAGACTCTCTGACTTTATAGTCCCTTTGACAGA 7794
Qy 146 -----SerIleAsn----- 148
Db 7795 TTTGAGATTCCATCAATTTGGATAAATCTTCAAAATGTTAAAGATGTTAAAAATCCCAATT 7854
Qy 149 Glu----- 149
Db 7855 GAGATTTTCCACTCCAGAAATTCACCTCTCTCAACACCTTCCGTGTCGTTCCTTTTACAAT 7914
Qy 150 -----GlyAsn-----Asn----- 152
Db 7915 TGACTTGTGGAATAAAGCAAAAGATCATTCGAATATCGACCAATGCTGAGCAGTGA 7974
Qy 153 -----Ile-----Ser 154
Db 7975 GCTACAGTGGCCTTTCCAGAGTGTATTGTGAGAGACCTGGAGATGTTGAACATTTCTCT 8034
Qy 155 -----LeuThr-----Cys-----Ile----- 158
Db 8035 TGCAAGACTCTCTCTGACAGACTTCCATGTACAGAAATCACAATTTCCAGAAATTCACAAT 8094
Qy 159 -----Ala-----ThrGly----- 161
Db 8095 CCCAATGTCAATCTCAAGATTTTACAGGTTCTGTATCTTCACATACAGAAATTCAGCT 8154
Qy 162 -----ArgProGlu 164
Db 8155 TCCTCACCTCTCATGCAAACTGAAATACCTGTTTCGGCAAACTACATAGCGTCTCTGAA 8214
Qy 165 -----Pro----- 165
Db 8215 AATCCAATCTCCCTCTTTTATATTATAGTGTAGTGCCAAACATACAGAACTAATCTACTTC 8274
Qy 165 ----- 165
Db 8275 AGAGAACAAAGCAGAGATTGTGGCTTCTGTCTGCTGCGCAGGAGAGTCCAAATTTGAGC 8334

Db 10492 GAATTTAAGGGTACTCGTCTTCAGTAAGTTTACAAGGAGCCTCTAATTTTGCTGGAT 10551
Qy 235 -----
Db 10552 CTGGAACCTTTGAAGTAGGAGAAATTTTGTCTGGAGAAGCTACTCTCCGACGCATCTATGG 10611
Qy 236 -----Gly-----Lys-----Gly-----
Db 10612 CACATGGGAACACATATGATTAACCAATTTACAGGTATTTACAGTACTTTTGACACAAAGG 10671
Qy 240 ---Thr---LeuGln-----
Db 10672 AAAACACATGACAGAGCCACCTAGAGCTCTCCCAATGGACCATGTCAACCCCTTCTACA 10731
Qy 243 ---CysGlu-----
Db 10732 GGTTCATGTGAGTCAACCCAGTCCCTCTTTGATCTCCATCAGTCTTTGACAGGAAGTGAAT 10791
Qy 244 -----
Db 10792 CCTGAACTAGCACTAAGAACCAAGAGGTGAGTGGGAAAAGTGGAGTCCAGGTGAATC 10851
Qy 245 ---Ala-----Ser-----
Db 10852 ACAGGTCTTTCAGCACAATGACACTTCTCCAATGACCAAGAAGAGTACGCCTTGACAT 10911
Qy 247 ---AlaVal-----
Db 10912 TGCTGGATCCTTAGAAGGACAGCTGTGGGACCTTGAAAATTTCTTTTACCGGCATTTGG 10971
Qy 248 -----
Db 10972 CAAGAGCTTGAGGAACTCTACAGATAGACGGAAGCGTCAGTATCTTCAAGCTTCGAC 11031
Qy 249 ---Pro-----Ser-----
Db 11032 TTCTCTTCACTATACAAAACCCGAATGGCTATCTCTCTCACTCCCTGTGCAAGAACT 11091
Qy 251 ---AlaGlu-----
Db 11092 GACTGATGATTCATTAACAGGGGCTGAAACTAAATGACTTTCAGTGGAAATCAAAATCTA 11151
Qy 253 ---Phe-----Gln-----
Db 11152 TAAGAAATTTAAGTACTTTCACCATTTTCCCTCAACCTTAACTAAGTCTCCCAAGTAAATTT 11211
Qy 255 ---Trp-----
Db 11212 CCTGGGGTTGATCTGTTAACACAATACTCTAAACGAGGGCTCTCTGTCCCTTACCTT 11271
Qy 256 -----Tyr-----Lys-----
Db 11272 TGAGACAACTATACCTGAAATTCATTAAGTCTGTCTCCAGTTTACCTTCCAAAGAGCTT 11331
Qy 257 -----
Db 11332 TCCCGTTGGCAACACTGTCTTTGATCTGAATAGCTAAACCACTAAATTCAGAGATTGA 11391
Qy 258 ---Asp-----AspLys-----
Db 11392 TCTGCCTAGTATACCCCTGCCAGAGACCAATTTGAGATCCCATTCCTTTGAGTCTCTGT 11451
Qy 261 -----Arg-----Leu 262
Db 11452 ACCTGCTGGATTTTATTTCCGTTCTTTGGAGAACTGACTGCACAGTTGGGATGGCTTC 11511
Qy 263 -----IleGlu-----
Db 11512 TCCCTGTATATGTACCGTGGAGCACTGGTTGGAAAAACAAAGCAGACCATGTTGAAC 11571
Qy 265 -----Gly-----Lys-----
Db 11572 ATTCTGGATTCACATGAGGTTCAACCTTGCAGTTTCTGGAGTATGCTCTAAAAGTTGT 11631

Qy 267 -----Lys-----
Db 11632 GGGAAACACACAGGATTTGAAAATGATTAAGTTTCACTATAAAATCAAAAGAAACACTTCAACA 11691
Qy 267 -----
Db 11692 CTGTGACTTCAATGTGAGTATTAACGAGAGTGTATATTTGAAGGACTTTTGGGACTTGA 11751
Qy 268 -----Gly-----
Db 11752 GGGAGAGGCTCATCTGGACATCACCAGCCAGCACTGACTGACTTCCATCTGCACTACAA 11811
Qy 269 ---Val-----
Db 11812 AGAAGACACAGCAAGTGTGTCTGGCTCAGCAGCGCTCCCAGAGCCATAGGCACTGTGAGTCT 11871
Qy 270 ---Lys-----
Db 11872 GGATGCAAGCACAGATGACCAGAGTGTGAGGCTGAATGTCTACTTCCGCCCTCAGTCCCC 11931
Qy 271 -----ValGlu-----
Db 11932 TCCAGATAATAAATCTCAGCATATTTCAAATGAGTGGAGGGCAAGAGAGTCTGATGTGA 11991
Qy 273 ---Asn-----Arg-----Pro-----
Db 11992 AACATACATCAAAATTAATCTGGGAAGAGAGCAGCTTTTCAGATTGCTAGACTCCCTAAA 12051
Qy 276 ---Phe-----Leu---SerLysLeuIle-----
Db 12052 AAGCAATGTGCCAAGGCTTCTGAGGCTGTTTATGATTATGTCAAGAA---GTACCACCT 12108
Qy 282 ---PhePhe-----
Db 12109 GGGACATGCTTCTTCAGAGCTAAGAAAAGTCTTCAGAAATGATGCTGAACAGCCATAAG 12168
Qy 283 -----
Db 12169 GATGTTGATGAGATGAACGTGATGCCAGAGGGTAAACCGTGATACCTACCAGAGTCT 12228
Qy 284 -----Asn-----
Db 12229 ATATAAGAAGATGTTGGCTCAGGAGAGCCAGAGTATCCTCGAGAAAATCAAGAAAATGGT 12288
Qy 285 Val-----SerGlu-----His-----Asp-----
Db 12289 GTTAGGAGTCTAGTATGATTACTCAGAGTACCACATGCGCAGTCAATGGCTGATGGA 12348
Qy 289 -----
Db 12349 CTCAGTCATTCATTTCCCTGAAGTTCAATAGAGTCCAGTTCACGAGGAATGCTGGAACATA 12408
Qy 290 ---Tyr-----GlyAsn-----
Db 12409 TACTGTGCAAGACTTTACATATAGCCATGAGGGNAACCAAGAAAGTTACTCTCTCAGCT 12468
Qy 293 ---Tyr-----Thr-----Cys-----ValalaSer 298
Db 12469 GTTTAATGGGTTAGGACACCTGTTTTCCTAATGTTCAAGACCAAGTAGAAGAAATCAAGAGT 12528
Qy 299 Asn-----Lys-----
Db 12529 AATCAATGACATAACATTTAAATGTCCCTTTTCCCAACACCTTTGTAAACTTAAAGAGTGT 12588
Qy 301 ---Leu-----Gly-----His-----Thr-----
Db 12589 CCTATTGATTTTTCAGGGAGGACTTAAACATTTTATCCAACTTAGCCCAACAGGATATCAA 12648
Qy 304 -----
Db 12649 TTTTACAACATACTAAGTGACTTTCAGAGCTTTTGGAGAGACTTTTAGACATCATAGA 12708

```
Qy 304 ----- 304
Db 12709 AGAAAAATGAATGCCTAAAGAACATGAATCTACTTGTGTCCTGATCATATCAACAT 12768
Qy 305 ----- 306
Db 12769 GTTCTTCAAAACACATCCATCCATTTGCATTTAAATCCCTGAGAGAAACATATACTCTGT 12828
Qy 307 ----- 309
Db 12829 CTTGAGTGAGTCAATGACTTTGTTCAATCCATATCTTCAAGAGGGGCTTATAAGCTTACA 12888
Qy 310 ----- 311
Db 12889 GCAGGTCCATCAGTATATGAGGCTTTCGTGAAGAGTATTTTGCATCCGAGTGCTGGTGG 12948
Qy 312 ----- 313
Db 12949 CTGACAGTAAATATTTATGAATAGAGAAAGATGTTGACCTTATCAAGACCTTTT 13008
Qy 313 ----- 313
Db 13009 GGCTCTCTGAGGATTTCTACTCTGAATACAGTGTGACAGCTGCTGATTTGCTTCCAA 13068
Qy 314 ----- 317
Db 13069 AATGTCAACTCAGTTGAGCAATTTGTGTCAGGGATATCAGAGATATCTTAGCATGCT 13128
Qy 318 ----- 318
Db 13129 TGCTGACATAAATGGAAGGGAGGAGAAAGTTGTCAGAGCTTTCTATTGTTGTAAGGA 13188
Qy 319 ----- 321
Db 13189 AAGATAAAGAGCTGGTCCACTGCGTGGTGGCGAATAATACGCTGATTACCTCCGCGAGCT 13248
Qy 322 ----- 322
Db 13249 CCATTCCAAATCGCAGGATTTTTCAGACCAGCTCTCTGGCTACTATGAAAAATTCGTTGC 13308
Qy 323 ----- 325
Db 13309 TGAGTCCACAAGACTGATGATGACCTGTCTCAATTCAAAACTACCAATGTTTCTCAGATACAT 13368
Qy 326 Arg ----- 328
Db 13369 CGCTGAGTTACTGAAAAAGCTGCAGGTGCGCCACAGCCCAATATGCGCTGCTGAAAAAGGG 13428
Qy 329 ----- 329
Db 13429 GGAATTTGAAGCTGCTGTAAGTTGGGATCGCCTCGCTCTACAATGAAGGCTTGTCTGT 13488
Qy 330 Val ----- 333
Db 13489 GTCGAGCAGGCTACGCGGAAGTGAATGGCTGAAGGCTCTCGCTTCTTTCAGCATGGA 13548
Qy 334 ----- 341
Db 13549 CGAGAGATTGAATATGGGTTTCAGACCCCTTATCTGGCTCTCCATCTGCCACCATGCTT 13608
Qy 342 ----- 344
Db 13609 CCGGAACTCAGGAGCTTCGCTGGCAAGAGGCTGCTGGGAAGCAGCAGCGCGCTT 13662

RESULT 16
AY321317
LOCUS AY321317 14278 bp mRNA linear HTC 16-JUL-2003
DEFINITION Rattus norvegicus Acl-060 mRNA, complete cds.
ACCESSION AY321317
VERSION AY321317.1 GI:32527694
KEYWORDS HTC.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
```

```
REFERENCE
AUTHORS Xu, C.S., Li, W.Q., Li, Y.C., Zhao, L.F., Ma, H., Wang, L., Wang, S.F., Han, H.P., Wang, G.P., Chai, L.Q., Yuan, J.Y., Yang, K.J., Yan, H.M., Chang, C.F., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.
TITLE Liver regeneration after PH
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 14278)
AUTHORS Xu, C.S., Li, W.Q., Li, Y.C., Zhao, L.F., Ma, H., Wang, L., Wang, S.F., Han, H.P., Wang, G.P., Chai, L.Q., Yuan, J.Y., Yang, K.J., Yan, H.M., Chang, C.F., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-2003) Henan Bioengineering Key Lab, Henan Normal University, NO. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R. China

FEATURES
source
1..14278
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
41..14272
/notes="liver regeneration related protein LRRG183"
/codon_start=1
/product="Acl-060"
/protein_id="AAP86249.1"
/db_xref="GI:32527695"
/translation="MGQRPALRAPLLLLFLFLDTSVWAQDATRFKHLRKVYSVE
AESSVRGTFADSRATKINCKVEVLPQVQTLIMRTSQCTLKEVGFNPEGKALMKK
TKNSFPAFASRYELKAPFEGKRVALYDLPGEPNYILNKRGIISALVSPETED
KQVLEDTVYNGCTQVTPNSRGKTATMSTERNLQHCDFQIPISVPLALIKGL
VRPLSTLSSSSCOVTLPRKRVSEACNEOHLPLFPYKNKYGMHTVTKLSLE
DTPKINSRPERGINOVGLAFESTKSTSPKQADAVLTKLQELKGLISFQNAQRL
FHKLVTELKLGSEATISLIPOLIEVSSPITLQALLQCCQPECTYHLWLKTEKAP
LLDIIYVLMALIPNPSVQLQEIFNTAKELQSRATLYALSHAVNSVITAMDRSRFP
LEDIAGYLMKQIDNECMQEDEDFTLIRLVGNMTRMVRVMPALKSVLNCVSTKPS
KLIQWQSEOVKNFVASHIANILNSRELYVODLPIKNAALVNSLILARSPSSDINKIA
LOKQAOLALRMEMGDEVITLFDPTFVNDVAPVEKRLAAYLLRSLTMDRFSRN
YQIKSVSIPLEDVPSAKLEGVLFDPPSSVLPKESMLKTLTVFGIASLDLFEILRG
KGFEIUEALFGKQGFPPSVNKAALYVNGQVDPVRSKVLVDHFGTKDKDKHQDWYN
GIMPIVDKILRILKGLFVRLQDLQVLGKLLNAGYKTLTGKIDRQVYKTLNKNRI
EIDPILPGLGKSKDLKVPESVTPALNFKSVGFHLPSQEVQIPTFTPTKTHQVPL
QMLVQALREGSKDILFHYIFMENAFELPTGVGLQQLQSSGVFTPGIKALVAGLELAN
IOALVAKPSVSLFVFMGIIIPDPAKGVQMTNPFHESGLEARVAKAGOLKVI
PSPKRVPLFGSNTLHLSTTTEVTPPIENRKSMTCKPFTGNVYCTTGAYSA
SSTESAYVLTGDTREYELKPTGEVBOYASATVELLKEDSLVDYTLAFVQAEV
QQSEATAFKINRSRILSSEVLIPGFVNFTILAVNDESKDKNTYKLLIDQNK
ITSVVGVHSYDKGDKGVGVSTPRLQARSEVHTLSWSTKLLFQDSSATATG
STLSKRVARYDNEKIEFDNTGTNVDTKVASNFVVDLSRYPRMVEYAGLLDHRV
PQDMPTRHMGSKLIYDHLNGLSELNLPKVLDPDHPDLNLFKTDGRVRYKTLNKNRI
EIDPILPGLGKSKDLKVPESVTPALNFKSVGFHLPSQEVQIPTFTPTKTHQVPL
GILGILSTVYSLNYSVSVTGNTSRDHFSLQAOVRMKADSVDFLPSYVQSGST
TYGKSTFTVYSCDGLHKLKELDSKFKVSHVEKFGNPPVSKLLTFETSSALGPMSAT
VQDSKQQLHYVQDKVQGFVSLIAGGEYGLSYERDSMTGMSGESNMENSTY
FQGTNQIVMGYQDMLSVTSDLDQGIKNTASLKYENYELTLKSDSSQOENFAAS
NKLDFTSKGALLRSEHQYKSLRVLTLGSLTSQVGLNADILGTDKINTFAHK
STLKAQGYSTGATNTKLSPLLENELNAGLSQSMKLSSTSGRFKEHKLHFDLSL
GRALTRVSGISYQAMILGADSKNPNFKLSREGLKLSNDMMGSAEMLKHTFSLR
ISGLSDPFSKEMNIYSGDKYKONENLOPYSGFITSNDLYKDALVTNNRGLLE
EPKLVNNGVNGKTYQNNLEKHYTISYIDLVAVSADTATVATVQGVFSEHRLNADLE
GLASSVDVTTYSDDPLHFNNTVFLAPFTLVGTDHTSDGKMSMGHEHTGYKSF
LLKAEPALATVSHDYKIGTSHNLLYKNSVSTALEHTLSALLTAEQTSWKFTSLND
KVTQSEPEAYNTDKIGIELSGRADLSGLSPIKVPFFYSEPVNVLNSLBNDAFDP
REFTDVAVKVDKQDVHTISLFPFQSLPDYLERNRGIISLEAMKEQLRSLSDQF
RETVRVALSLPQIHDYLNASDWERQVAGAKLTSFMEYRITONDVLIALDSAKI
NMEKUSQLETYALQFDQYIRDNDAQDLKRTIAQIIDRLIEKLMDEQHYHRYNLA
KSHNLYLVFENVDMNQISSGASWQNTVKYQIRIQIEKHLQHLRQTLHNHIDTQFL
AAELKQIIEALDVPMLDQLRTAILFQRIISVIERVKYFMNLTEDEKFKTEKIPV
IVRELIEKYVDROIQVIMELNRLSDMSVKLKAQDFYHOFVDTKNSKIQETIKDYDKLVGT
DDTVETIKAVSFENIIEELNRLSDMSVKLKAQDFYHOFVDTKNSKIQETIKDYDKLVGT
ALELPQTEALKLVEDPFTVNSLEKDKTKVTVVDMLODGLAQIKAQFQDALED
VRDRIQMDIQGELERCLSVSVITVTTISDWNTWLTAKNTIDFQEQTSQKWAAS
VKALVEQGFIVPEITQTFLMTPAFENSHALQEANFQTPDFIVELTDLIRLPSIWINFK
```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 14278)

Xu, C.S., Li, W.Q., Li, Y.C., Zhao, L.F., Ma, H., Wang, L., Wang, S.F., Han, H.P., Wang, G.P., Chai, L.Q., Yuan, J.Y., Yang, K.J., Yan, H.M., Chang, C.F., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.

Liver regeneration after PH

Unpublished

2 (bases 1 to 14278)

Xu, C.S., Li, W.Q., Li, Y.C., Zhao, L.F., Ma, H., Wang, L., Wang, S.F., Han, H.P., Wang, G.P., Chai, L.Q., Yuan, J.Y., Yang, K.J., Yan, H.M., Chang, C.F., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.

Direct Submission

Submitted (11-JUN-2003) Henan Bioengineering Key Lab, Henan Normal University, NO. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R. China

Location/Qualifiers

1..14278

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

41..14272

/notes="liver regeneration related protein LRRG183"

/codon_start=1

/product="Acl-060"

/protein_id="AAP86249.1"

/db_xref="GI:32527695"

/translation="MGQRPALRAPLLLLFLFLDTSVWAQDATRFKHLRKVYSVE
AESSVRGTFADSRATKINCKVEVLPQVQTLIMRTSQCTLKEVGFNPEGKALMKK
TKNSFPAFASRYELKAPFEGKRVALYDLPGEPNYILNKRGIISALVSPETED
KQVLEDTVYNGCTQVTPNSRGKTATMSTERNLQHCDFQIPISVPLALIKGL
VRPLSTLSSSSCOVTLPRKRVSEACNEOHLPLFPYKNKYGMHTVTKLSLE
DTPKINSRPERGINOVGLAFESTKSTSPKQADAVLTKLQELKGLISFQNAQRL
FHKLVTELKLGSEATISLIPOLIEVSSPITLQALLQCCQPECTYHLWLKTEKAP
LLDIIYVLMALIPNPSVQLQEIFNTAKELQSRATLYALSHAVNSVITAMDRSRFP
LEDIAGYLMKQIDNECMQEDEDFTLIRLVGNMTRMVRVMPALKSVLNCVSTKPS
KLIQWQSEOVKNFVASHIANILNSRELYVODLPIKNAALVNSLILARSPSSDINKIA
LOKQAOLALRMEMGDEVITLFDPTFVNDVAPVEKRLAAYLLRSLTMDRFSRN
YQIKSVSIPLEDVPSAKLEGVLFDPPSSVLPKESMLKTLTVFGIASLDLFEILRG
KGFEIUEALFGKQGFPPSVNKAALYVNGQVDPVRSKVLVDHFGTKDKDKHQDWYN
GIMPIVDKILRILKGLFVRLQDLQVLGKLLNAGYKTLTGKIDRQVYKTLNKNRI
EIDPILPGLGKSKDLKVPESVTPALNFKSVGFHLPSQEVQIPTFTPTKTHQVPL
QMLVQALREGSKDILFHYIFMENAFELPTGVGLQQLQSSGVFTPGIKALVAGLELAN
IOALVAKPSVSLFVFMGIIIPDPAKGVQMTNPFHESGLEARVAKAGOLKVI
PSPKRVPLFGSNTLHLSTTTEVTPPIENRKSMTCKPFTGNVYCTTGAYSA
SSTESAYVLTGDTREYELKPTGEVBOYASATVELLKEDSLVDYTLAFVQAEV
QQSEATAFKINRSRILSSEVLIPGFVNFTILAVNDESKDKNTYKLLIDQNK
ITSVVGVHSYDKGDKGVGVSTPRLQARSEVHTLSWSTKLLFQDSSATATG
STLSKRVARYDNEKIEFDNTGTNVDTKVASNFVVDLSRYPRMVEYAGLLDHRV
PQDMPTRHMGSKLIYDHLNGLSELNLPKVLDPDHPDLNLFKTDGRVRYKTLNKNRI
EIDPILPGLGKSKDLKVPESVTPALNFKSVGFHLPSQEVQIPTFTPTKTHQVPL
GILGILSTVYSLNYSVSVTGNTSRDHFSLQAOVRMKADSVDFLPSYVQSGST
TYGKSTFTVYSCDGLHKLKELDSKFKVSHVEKFGNPPVSKLLTFETSSALGPMSAT
VQDSKQQLHYVQDKVQGFVSLIAGGEYGLSYERDSMTGMSGESNMENSTY
FQGTNQIVMGYQDMLSVTSDLDQGIKNTASLKYENYELTLKSDSSQOENFAAS
NKLDFTSKGALLRSEHQYKSLRVLTLGSLTSQVGLNADILGTDKINTFAHK
STLKAQGYSTGATNTKLSPLLENELNAGLSQSMKLSSTSGRFKEHKLHFDLSL
GRALTRVSGISYQAMILGADSKNPNFKLSREGLKLSNDMMGSAEMLKHTFSLR
ISGLSDPFSKEMNIYSGDKYKONENLOPYSGFITSNDLYKDALVTNNRGLLE
EPKLVNNGVNGKTYQNNLEKHYTISYIDLVAVSADTATVATVQGVFSEHRLNADLE
GLASSVDVTTYSDDPLHFNNTVFLAPFTLVGTDHTSDGKMSMGHEHTGYKSF
LLKAEPALATVSHDYKIGTSHNLLYKNSVSTALEHTLSALLTAEQTSWKFTSLND
KVTQSEPEAYNTDKIGIELSGRADLSGLSPIKVPFFYSEPVNVLNSLBNDAFDP
REFTDVAVKVDKQDVHTISLFPFQSLPDYLERNRGIISLEAMKEQLRSLSDQF
RETVRVALSLPQIHDYLNASDWERQVAGAKLTSFMEYRITONDVLIALDSAKI
NMEKUSQLETYALQFDQYIRDNDAQDLKRTIAQIIDRLIEKLMDEQHYHRYNLA
KSHNLYLVFENVDMNQISSGASWQNTVKYQIRIQIEKHLQHLRQTLHNHIDTQFL
AAELKQIIEALDVPMLDQLRTAILFQRIISVIERVKYFMNLTEDEKFKTEKIPV
IVRELIEKYVDROIQVIMELNRLSDMSVKLKAQDFYHOFVDTKNSKIQETIKDYDKLVGT
DDTVETIKAVSFENIIEELNRLSDMSVKLKAQDFYHOFVDTKNSKIQETIKDYDKLVGT
ALELPQTEALKLVEDPFTVNSLEKDKTKVTVVDMLODGLAQIKAQFQDALED
VRDRIQMDIQGELERCLSVSVITVTTISDWNTWLTAKNTIDFQEQTSQKWAAS
VKALVEQGFIVPEITQTFLMTPAFENSHALQEANFQTPDFIVELTDLIRLPSIWINFK

MLKNVILPFLSTPEFTLLNFRVRSFTIDLLLEIKAKIIRTIIDOMLSSELOWPLPEVY
 LRDEMYNISLARSPLDPFVPRITITPEFTIPVNLKDLQVPLDHLHPEFOLPHLSCTT
 EIPAFGLKHLVILKQSLPFLDASANTQNIITSENKARIIVASVTARGESFEALNEDF
 QAQAFLELNLNPLVLAKESVNFSSKVMHEGKILVSGKALEGKSDTVARLHTEKNT
 VENGIVLVKINNOFTLDSQTKYFPHKLSVPRFLDPSKASLNNEIKTLLEAGHMAWTS
 GTGSMWACPNFSDGHSKISFIVDGPASFGLSNINNGKHLRVQKLTSLRSGLFN
 YSRFEVSKVSHGSSVILTAERALLGDKAEAMTEGHANLNGKVLTKNSLFPFS
 AQOPEITASTNENLKVSPPLKLTGKIDFLNVALPLSPAQAQASWOLSTRPNQVYK
 NONFSAIINNHMEASIVMGDANLPLNPLIPIPEINLPTFTFTPLLKDFPSIMEET
 GLKEFTKTQSDLSLKAQKKNRDKHSVVILPKMYEFELMANVNSWDFEKFVRDN
 ALHFTASYNETKIKDKYKATENSLSQPSRTFQNRGHTIPLVNIIEVSPFAETLASH
 VIKRARTSPVTPGPNIIIVPSYRLVPLSLQVLFPHIPLTFLKFSFDFPKLSTIDNI
 YIPAMGNFTYDFKSSVITLNTNAGLNQSDLVAREFLSSSFVTDALQVLYKLSRNL
 MRKVLKATAVSLTNKFLGSHDSTLSLTKNMEASVKTANLHAPIFTMNEKOSLN
 GNTKSPVTSSSIELNDFNSKLHSAAGGVDPKPSLSLSLSLSLSLSLSLSLSLSLS
 FLSOYSGSVANAVYNSKGTSSVRLQASNPAGIWNFEVGENFAGATUURLYG
 TWEHNLINHLQVSEYDYGKQTCRAILELSPWMTSLQVHVSQSPFLDLHFFQOE
 VILKASTNOKVSKSEVOVESQVLOHNAHFNDSQBEVRDLDSLEGLMDLENFL
 PAFKSLRELLQIDGKRYLOASTSLHYTKNPNGYLLSPVQBLTDRFIIPGLKDNF
 SGIKYIKLSTSPALNLTMLPKVFPVGLDLPVTOYKPEGSSVPTFTTIPETQLTVS
 QFTLPKSPVGNVFDNLKLTNLIADVDLPSITLPTOTIEIPSLSESVAGIPIPFPG
 ELTAHVGMASPLNVMTWSTGKKNKADHVEFLDSTCSLQFLLEYALKVGVHRIEND
 KFTYKIKGTLQHCDFNVKYNEDGIFGLMDLEGEALHDITSPLTDLHLYKEDTYSV
 SASAASPAGTIVSLDASTDQSVRLNAVYFRQSPDPNKLKSIPOEWRDKESEDGETYIK
 INWEEAARFLDLSLNVPKASEAVYVYKHYHLGHASSELKSLQNDASHAIRVVD
 EMVNAQVRTRDTYQSLYKMLAQESQSIPEKLMVGLSLVRIITOKYHMAVTLWMS
 VHLKFNVRVQFNGAGTYVDELYTIAMRETKKLSQLFNGLGHFSYVQDOVKRS
 VINDIYFKPFPSPCKLDVLLIPREDINILNLGQDINFTTILSDQSFLERLLD
 LIEETKLNNESTCVPHIHNPFKTHIPFAKSLRENIYSVSEFNDPVSQISLEG
 SYKLOQVQYMKAFREYDPSVVGWITKYELEKQVLDLITLAPLAPDFVSEYSVT
 AADFAKSTQEQVRSRDIREYLSMLADINGKREKVAELSIIVVKERIKSWSVAE
 ITSDYLRQSHLSKLDQSDQSYGFEKFAESTRLIDLSIQNHMFURYIAELLKQLOV
 ATANNGLKRGDFEAAVGLACLYNEGLSVDEAVAVNGLKASRFFSMDSVCLNWS
 DPFILWLSICPPCFKLRDPAGKCAQALAKADKAGSOLGLEKAFSESVCQLPQA
 SOAVNKQOIFSVOKGLSDTVRYILIGWLEVAPMKDFTSLCHLTVCCVCRQKIV
 PRYKQLLGLGACMVICTWISKEILLTIREAVRLTNTYIKOLVRKRIIISALBGKI
 RPTVVDYKEVLLTLPVTPRTQYLCSEFLCELTLVSVYTPAHLASALLARLHMGOTQ
 P"

ORIGIN

Alignment Scores:		3,06e-12	Length: 14278
Pred. No.:	Score:	1684.30	Matches: 295
Percent Similarity:		10.10%	Conservative: 40
Best Local Similarity:		8.89%	Mismatches: 6
Query Match:		69.95%	Indels: 2977
DB:		11	Gaps: 262
US-10-017-084A-523 (1-344) x AY321317 (1-14278)			
QY	1 Met	---LysThr---Ile	-----Gln----- 5
DB	3718	CTCAGAGTTGAACCTCCCAAGAGTGGGATGGCCAGACTTCCATATCCAGACACACCTCTT	3777
QY	6 ProLys		-----MetHis----- 9
DB	3778	CCTAAAAACTGATGGCCGAGTCAATATACACTAAACAAAGACAGAAATAGAGATTGACAT	3837
QY	9	-----	----- 9
DB	3838	TCCTTTGCTTTGGGTGGCAAGTCTTCAAAAGACCTCAAGGTGCCAGAAAGTGTGAGGAC	3897
QY	9	-----	----- 9
DB	3898	ACCAGCCCTCAACTTCAAGTCTGTGGGGTTCCATCTGCGGTCTCAAGAGTCCAGATTCC	3957
QY	10	-----Asn-----	-----Ser----- 11
DB	3958	CACCTTTTCAATCCCCAAGACACATCAGCTGCAAGTGCCTCTCTTTGGGCAATTCGACCT	4017
QY	12	-----IleSer-----	-----Trp----- 14
DB	4018	TTCCCAAAATGCTACAGCAACTTGTGACAACTGGTGCAGTCTCCTACATCGGTGGCAACAC	4077

QY	14	-----	----- 14
DB	4078	CAGCAGGGATCACTTTCAGCCTTCAGTCCAGTACCGCATGAAGGCTGACTCTCTGTGGTTGA	4137
QY	15	-----Ala-----	-----Ile 16
DB	4138	CTGTGTTTCTCTACAGTGTGCAAGGATCTGGAGAAACAACATACGACGACGAAGACACATT	4197
QY	17	-----Phe-----Thr-----	----- 18
DB	4198	CACCTTATCGTGTGATGGGTCTCTACATCATATAATTTCTAGATTCATAATTCAGATCAG	4257
QY	18	-----	----- 18
DB	4258	CCACGTAGAAAAATTTGGAAAAACAACCCAGCTCTCGAAAGGTTTATTAACTTTGAAACATC	4317
QY	19	-----Gly-----Leu-----AlaAlaLeu-----	----- 23
DB	4318	TAGTGCTTTGGGACCAACAGATGTCTGTACAGTTTCAGCTGGACTCAAAAAAGAAACAAC	4377
QY	24	-----Cys-----	----- 24
DB	4378	TCTGTATGTCAAAGACATCAAGGTTGACGGACAGTTCAGAGTATTTTCATTGTACGCTCA	4437
QY	25	-----Leu-----Phe-----	----- 26
DB	4438	AGGTGAATATGCGCTGTCTTATGAGAGAGATTCTATGACTGGCCAGATGAGCGGAGAATC	4497
QY	27	-----	-----Gly---ValPro 30
DB	4498	CAACATGAATTTAACTCCACCTACTTCCAGGGGACCAACACAGATAGTGGGAATGTACCA	4557
QY	31	-----Val-----	-----Arg----- 32
DB	4558	GGATGGAATGCTGTCTGTCTCACTTCCACCTCTGACCTGCAAGTGCATATTCAGAGAAC	4617
QY	33	-----Ser-----	----- 33
DB	4618	AGCTTCCCTTAAATATGAAACTATGAGTTGACTCTGAAATCCGACAGTGGGCGAGTA	4677
QY	34	-----Gly---Asp-----	----- 35
DB	4678	TGAGAACTTTGCTGCTTCCAAACAGCTGGACATGACCTTCTTAAGAAAGGCGACTGCT	4737
QY	36	Ala-----Thr-----	----- 37
DB	4738	GGTTTCTGAACACACAGGCGCAACTACAAGTCCCTGAGACTTGTCAACCTTCTTCTGGATC	4797
QY	38	-----PhePro-----Lys-----	----- 40
DB	4798	CCTCACTTCCCAAGGTGTAGAAATTAATGCTGACATCTTGGGCGACCGACAAAATTAATAC	4857
QY	41	-----AlaMetAsp-----	-----Asn--- 44
DB	4858	TGGTCTCACAAGTCAACGCTAAAGATTGCACAGATGGAGTATCTACCTAGTGCACACAC	4917
QY	45	-----Val-----Thr-----Val---ArgGln-----	----- 49
DB	4918	CAACTTAAAGTACAGCCCGCTGCTGCTGGAGATGAGTTGAACGCGAGACTTGGGCTCTC	4977
QY	50	-----Gly-----	----- 50
DB	4978	TGGGGCATCCATGAATTTGTCAACAGTGGCGGCTTCAAGAAACACCATGCAAAATTCAG	5037
QY	51	-----GluSer-----AlaThr-----Leu-----	----- 55
DB	5038	TCTTGATGGGAGAGTGCCTCCTCAGAGGTATCACTGGGAGCATTTACACAGGCGCATGAT	5097
QY	56	-----Arg-----Cys-----Thr-----	----- 58
DB	5098	TCTGGTGCAGACGACCAAAAATGTCTTCAACTTCAAACTCAGCCGAGAGGACTGAAGCT	5157

```
QY 59 Ile-----Asp-----Asn-----Arg----- 62
||| ||| ||| |||
Db 5158 ATCAATGACATGATGGGCTCTACGCTGAAATGAAACTGGACCACACACAGTCTGAG 5217
QY 62
Db 5218 AATTTCCAGGTCTCTCCCTGGACTTCTTCTCAAAAATGGACAATATTTACAGTGGAGACAA 5277
QY 63 Val-----Thr----- 64
||| ||| |||
Db 5278 GTTTTATAAGCAGAAATTTTAACTTACAGCTACAGCCCTATTTCTTTTGGAAATTAATTTAAG 5337
QY 65
Db 5338 CAATGATCGAAATATGATCTCTAGTTTGTACCAAAATGGAGGTACGGCTGGAACC 5397
QY 67 ---Ala-----Trp-----Leu-----Asn----- 70
||| ||| ||| ||| |||
Db 5398 ACTGAAGCTGAATGTGGGTGGCAACTTTAAGGGAACCTACCAAAATAATGAGCTGAAACA 5457
QY 71 ---Ser-----Arg----- 72
||| ||| ||| |||
Db 5458 CATCTATACCATCTCTATTAAGCTGACCTGTGTAGTACAGGTTACAGAGCAGACACTGAGC 5517
QY 73 ---Thr-----Ile----- 74
||| ||| |||
Db 5518 TACGGTTCAGGGTGTGGAGTTCAGCCATAGGCTAAATGCAGACATCGAAGGCTGGCTTC 5577
QY 75 Leu-----Tyr-----Ala----- 77
||| ||| ||| |||
Db 5578 CTCGGTGTGATCTACTACCAGCTACAGTTCAGATCCCACTGCAATTTAAACAATGTTTCCG 5637
QY 78 ---Gly-----Asn----- 79
||| ||| ||| |||
Db 5638 CTTTGTCTGGCACCGTTTACCTTGGCGTCGCACACACATACAGTGGTGATGGGAAAT 5697
QY 79
Db 5698 GTCCCTCTGGGAGAACACACTGGGAGAGTACAGTAATTTCTGTGAAAGCAGAAC 5757
QY 79
Db 5758 TCTGGCACTTACCTTCTCATGACTACAAAGGATCCAGGCCACAATCTCTGTACAA 5817
QY 79
Db 5818 GAACAGGTCAGTACAGCTCTTGAGCACACACTCAGTGCCTTCTGCTGACTCCAGCTGAACA 5877
QY 80 AspLys----- 81
||| ||| ||| |||
Db 5878 GACAAGCAGCTGGAATTCAGAGCCAGCCTGAATGACAAAGTATACAGCCAGGAATTTGA 5937
QY 82 ---Trp----- 82
||| ||| |||
Db 5938 AGCCTACAACACTAAAGACAAAATTGGTATCGAGCTTAGTGGACGGGCTGACCTCTGG 5997
QY 83 ---Cys----- 83
||| ||| |||
Db 5998 GCTGTACTCTCCAATTAAAGTGGGTTTCTACAGTGGCCCTGTCAATGTTCTTAAATAG 6057
QY 84 Leu-----Asp-----ProArgVal----- 88
||| ||| ||| ||| ||| ||| |||
Db 6058 CTTGGAGATAAATGATGCGCTTTGACGAGCCCGGAGAATTCACAATGATGCTGTGTGAA 6117
QY 89 ---ValLeu----- 90
||| ||| ||| |||
Db 6118 ATAGATAAGAACCAAGATGTCACACTATACGCTTCCCAATCTTCCAAAGCCTGCCAGA 6177
QY 91 Leu-----Ser-----Asn-----Thr----- 94
||| ||| ||| ||| |||
Db 6178 TTATTTGGAGAGAAATCGAAGAGGAATTAAGTCTACTGGAGGCAATGAGGGGAAT 6237
QY 95 ---Gln-----Thr-----Gln----- 97
||| ||| ||| ||| |||
```

```
Db 6238 ACAAGCCCTCAGTGTGTGATCAGTTTGTGAGAAATATAGAGTGGCCCTCAGCAGGCTTCC 6297
||| ||| ||| |||
QY 98 ---TyrSer-----Ile-----Glu----- 101
||| ||| ||| ||| |||
Db 6298 TCAGCAGATTCATGATTAATCTGAATGCACTGCTGGGAGAGACAAAGTAGTGGTGCCAA 6357
QY 102 ---Ile----- 102
||| ||| |||
Db 6358 GGAAAATTAACCTTCTTCATGGAAAACCTATAGAATTAAGATAATGATGTAATAATGC 6417
QY 103 ---GlnAsn----- 104
||| ||| ||| |||
Db 6418 CTTAGATAGTGCAAAATCAACTTGAATGAAAACCTCTCAACTTGAGACATACCGAT 6477
QY 105 ---Val----- 105
||| ||| ||| |||
Db 6478 ACAATTTGATCAGTATATTAGAGATAAATTATGATGCACAGGACTTAAAAAGAACTATTGC 6537
QY 106 ---Asp-----Val-----Tyr----- 108
||| ||| ||| ||| |||
Db 6538 TCAGATTATTGATAGAAATCAITTTGAAAAGCTAAAAATGCTTGACGACAGTATCATATCCG 6597
QY 108 --- 108
Db 6598 TGTAAATCTAGCAAAATCAATCCATAAATCTCTATTATTATTGTTGAAAATGTTGATCTTAA 6657
QY 109 ---Asp-----GluGly----- 111
||| ||| ||| ||| |||
Db 6658 CCAAATCAGTAGTAGTGTGCGTCTTGGATCCAAAATGTGGATATCCAAATATCAAAATCAG 6717
QY 111 --- 111
Db 6718 AATCCAGATACAAGAAAAAACTCCAGCATCTCAGAACACAGATTCAATAATATAGACATTCA 6777
QY 111 --- 111
Db 6778 ACAGCTTGTGCAGAGTTAAACACAGATTGAAGCTCTTGATGTCCCAATGCAITTTAGA 6837
QY 112 ---Pro----- 112
||| ||| |||
Db 6838 TCAACTGAGAACTGCAATTTCTATTCCAAAGAAATAAGTGTCAITATTGAGCGTGTCAAATA 6897
QY 112 --- 112
Db 6898 CTTTGTATTGAATCTTATTGAAAGATTTTAAAGTAAGTGAAGAAAATCAATPCTTTTAGAGT 6957
QY 113 Tyr----- 113
||| ||| |||
Db 6958 TATAGTCCGTGAGTTAATTGAGAAATATGCAAGTAGACCGACAAAATCCAGGTTTATATGA 7017
QY 113 --- 113
Db 7018 TAAATCAATAGAGTTGGCCCAACAGATACAGCCTGAGTGAGCGCTCTTCAGAAAATAGATAA 7077
QY 114 ---Thr----- 114
||| ||| |||
Db 7078 TGTGCTACAGCAAAATTGAGATAAAGACTACTATGATAAATTTGGTTGTTTATTGATGA 7137
QY 115 ---Cys-----SerVal-----Gln-----Thr----- 119
||| ||| ||| ||| ||| ||| |||
Db 7138 CACTGTGAGTGGATTAAAGCAGTGTCTTTCAAAAATATCAITTTGAAGAACTGAATAGATT 7197
QY 119 --- 119
Db 7198 GATTGACATGTCGGTGAATAAAGCTTTGAAGCCTTTTGATTATCACCAGTTTGTAGACAAAAC 7257
QY 120 ---Asp----- 120
||| ||| |||
Db 7258 CAACAGCAAAATCCCGTGAGATGACTCAGAGAAATCAATGCTGAATCCAAAGCTCTCGAAT 7317
QY 121 ---AsnHis----- 122
||| ||| ||| ||| |||
```



```
QY 213 -----Arg-----ArgVal 215
Db 9532 TTCTGGGACAGAAATTTGAGAAAGTCAGAGCAATGCAATTACATTTCTTACCGCATC 9591
QY 216 -----Lys-----Val----- 217
Db 9592 CTATATGAACACAAAATTAAGTTTGATTAAGTACAAAACGTGAAATTCCTCAATCAGCC 9651
QY 218 -----Thr-----Val----- 219
Db 9652 TTCCAGGACCTTTCAAATCGTGGACACACTATCCAGTTCTCAACATTAAGTGTCTCC 9711
QY 219 ----- 219
Db 9712 ATTGTGCTAGACACACTGGCTTCCAGCCATGTGATCCCGAAGAAATCGGCACCCCAAG 9771
QY 220 -----Asn----- 220
Db 9772 CGTCACAAATTCAGGTCCTAACATCATTTGTCCTTCATACAGGTTAGTGTGCGGTCTCT 9831
QY 221 -----TyrPro----- 222
Db 9832 ACAGTTGCCAGTTTTCATATCCCTAGGACTCTATTCAAAGTTTTCCTCCACAGATTCAA 9891
QY 222 ----- 222
Db 9892 GAAATTAAGCACTATTGACAAATATTATATCCAGCCATGGGCAATTTACCTATGACTT 9951
QY 223 ----- 223
Db 9952 TTCTTTTAAATCAAGTGTATCATCACTCACTGAATACCAATGTGGACTTTTATAACCAATCAGA 10011
QY 224 -----Pro----- 224
Db 10012 TCTCGTGTGCTGTTTTTCTTCTCTTCATTTGTACGGATGCGCTGCGATACAAACT 10071
QY 225 -----TyrIle----- 225
Db 10072 AGAGGTATCATCAGTCTGATGCGGAAAGAAAGTATTGAAGTTAGCCACCGCTCTCTCT 10131
QY 226 -----SerGlu----- 226
Db 10132 AACTAACAAATTTTAAAGGGAAGTCATGACAGCACCATTAGCTTAACCAAGAAACAT 10191
QY 227 ----- 227
Db 10192 GGAAGCTTCAGTGAACAACTGCAACCTCCACGCTCCCATTTTCAATGAACCTTCAA 10251
QY 228 -----Ala----- 228
Db 10252 GCAGGAACTTAACGGAACACCAAGTCAAGCCCACTGTCTCATCTCCCTCCATTGAACATAA 10311
QY 229 -----Lys----- 229
Db 10312 CTATGACTTCAATTCCTCAAAGCTGCACCTGTCAGCAAAAGAGGTGTTGATCACAAGTT 10371
QY 230 Gly-----ThrGly-----ValPro 234
Db 10432 GGGTTCGTTCTTTCACAGGATATTTCAGGAAGTGTGCGCAATGAGCGAATGTGTACCT 10491
QY 235 -----Val----- 235
Db 10492 GAATTTCAAGGTACTCGGTCTTCAGTAAGGTTTCAAGAGGAGCTCTAAATTTTGCTGGAT 10551
QY 236 -----Gly-----Lys-----Gly----- 239
Db 10552 CTGGAACCTTTGAAGTAGAGAAATTTTGTGGAGAAAGTACTCTCTCGACGCATCTAAG 10611
QY 237 ----- 237
Db 10612 GAGTGGGACACAAATATGATTAACCAATTTACAGTATTTCAGCTACTTTGACACAAAGG 10671
QY 240 -----Thr-----LeuGln----- 242
Db 10672 AAAACAAACATGACAGAGCACCTAGAGCTCTCCCATGAGCAATGTCAACCTTCTACA 10731
QY 243 -----CysGlu----- 244
Db 10732 GGTTCATGTAGTCAACCCAGTCCCTCTTTGATCTCCATCACTTTGACAGGAAGTGTAT 10791
QY 244 ----- 244
Db 10792 CCTGAAAGTAGCACTAAGAACCCAGNAGTCAAGTGGAAAGTGAAGTCCAGGTTGAATC 10851
QY 245 -----Ala-----Ser----- 246
Db 10852 ACAGGTTCTTCAGCACAATGACACACTTCTCAATGACCAAGAAGAAGTACGCTTTGACAT 10911
QY 247 -----AlaVal----- 248
Db 10912 TGCTGATCCTTAGAAGAGCAGCTGTGGACCTTGAAATTTCTTCTACCGCATTTGG 10971
QY 248 ----- 248
Db 10972 CAAGAGCTTGAAGGAACTCTACAGATAGAGGAAGCGTCAGTATCTTCAAGCTTCGAC 11031
QY 249 -----Pro-----Ser----- 250
Db 11032 TTCTCTTCACTATACCAAAACCCGAATGGCTATCTCTCTCACTCCCTGTGCAAGAACT 11091
QY 251 -----AlaGlu----- 252
Db 11092 GACTGATAGATTCATTTATACAGGGCTGAACTAATAGATTCAGTGGATCAMAATCTA 11151
QY 253 -----Phe-----Gln----- 254
Db 11152 TAAGAAATTAAGTACTTCACTCCATTTGCGCTCAACCTTAACAATGCTCCCAAGTAAAT 11211
QY 255 -----Trp----- 255
Db 11212 CCTGGGGTTGATCTGTTAAACAACTACTTAACCCAGAGGGCTCCTGTGCTCCCTACCTT 11271
QY 256 -----Tyr-----Lys----- 257
Db 11272 TGAGCAACTATACCTGAAATTCATTAATTAAGTGTGCTCCAGTTTACACTTCCAAAGAGCTT 11331
QY 257 ----- 257
Db 11332 TCCGTTGGCAACACTGTCTTTGATCTGAATAAGCTTAACCACTAATTCAGATGTTGA 11391
QY 258 -----Asp-----AspLys----- 260
Db 11392 TCTGCTAGTATCACCTGCCAGAGCAGACCATTAAGATGCCATCCCTGAGTCTCTCT 11451
QY 261 -----Arg-----Leu 262
Db 11452 ACCTGCTGGGATTTTATTCGTTCTTTGGAGNACTGACTGCACAGTTGGGATGCGCTC 11511
QY 263 -----IleGlu----- 264
Db 11512 TCCCTGTATATGTCACGTGGAGCAGCTGTTGMAAAACAAAGCAGACCATGTTGAAAC 11571
QY 265 -----Gly-----Lys----- 266
Db 11572 ATTCTGSAATCCATGCACTGTTCACTTGCAGTTTCTGGAGTATGCTCTAAAGTTGT 11631
QY 267 -----Lys----- 267
Db 11632 GGSAAACACACAGGATGAAATATGATTAAGTTTATTAATCAAGGAACACTTCAACA 11691
QY 268 ----- 268
Db 269 ----- 269
```

```
Db 10612 CACATGGGACACAAATATGATTAACCAATTTACAGTATTTCAGCTACTTTGACACAAAGG 10671
QY 240 -----Thr-----LeuGln----- 242
Db 10672 AAAACAAACATGACAGAGCACCTAGAGCTCTCCCATGAGCAATGTCAACCTTCTACA 10731
QY 243 -----CysGlu----- 244
Db 10732 GGTTCATGTAGTCAACCCAGTCCCTCTTTGATCTCCATCACTTTGACAGGAAGTGTAT 10791
QY 244 ----- 244
Db 10792 CCTGAAAGTAGCACTAAGAACCCAGNAGTCAAGTGGAAAGTGAAGTCCAGGTTGAATC 10851
QY 245 -----Ala-----Ser----- 246
Db 10852 ACAGGTTCTTCAGCACAATGACACACTTCTCAATGACCAAGAAGAAGTACGCTTTGACAT 10911
QY 247 -----AlaVal----- 248
Db 10912 TGCTGATCCTTAGAAGAGCAGCTGTGGACCTTGAAATTTCTTCTACCGCATTTGG 10971
QY 248 ----- 248
Db 10972 CAAGAGCTTGAAGGAACTCTACAGATAGAGGAAGCGTCAGTATCTTCAAGCTTCGAC 11031
QY 249 -----Pro-----Ser----- 250
Db 11032 TTCTCTTCACTATACCAAAACCCGAATGGCTATCTCTCTCACTCCCTGTGCAAGAACT 11091
QY 251 -----AlaGlu----- 252
Db 11092 GACTGATAGATTCATTTATACAGGGCTGAACTAATAGATTCAGTGGATCAMAATCTA 11151
QY 253 -----Phe-----Gln----- 254
Db 11152 TAAGAAATTAAGTACTTCACTCCATTTGCGCTCAACCTTAACAATGCTCCCAAGTAAAT 11211
QY 255 -----Trp----- 255
Db 11212 CCTGGGGTTGATCTGTTAAACAACTACTTAACCCAGAGGGCTCCTGTGCTCCCTACCTT 11271
QY 256 -----Tyr-----Lys----- 257
Db 11272 TGAGCAACTATACCTGAAATTCATTAATTAAGTGTGCTCCAGTTTACACTTCCAAAGAGCTT 11331
QY 257 ----- 257
Db 11332 TCCGTTGGCAACACTGTCTTTGATCTGAATAAGCTTAACCACTAATTCAGATGTTGA 11391
QY 258 -----Asp-----AspLys----- 260
Db 11392 TCTGCTAGTATCACCTGCCAGAGCAGACCATTAAGATGCCATCCCTGAGTCTCTCT 11451
QY 261 -----Arg-----Leu 262
Db 11452 ACCTGCTGGGATTTTATTCGTTCTTTGGAGNACTGACTGCACAGTTGGGATGCGCTC 11511
QY 263 -----IleGlu----- 264
Db 11512 TCCCTGTATATGTCACGTGGAGCAGCTGTTGMAAAACAAAGCAGACCATGTTGAAAC 11571
QY 265 -----Gly-----Lys----- 266
Db 11572 ATTCTGSAATCCATGCACTGTTCACTTGCAGTTTCTGGAGTATGCTCTAAAGTTGT 11631
QY 267 -----Lys----- 267
Db 11632 GGSAAACACACAGGATGAAATATGATTAAGTTTATTAATCAAGGAACACTTCAACA 11691
QY 268 ----- 268
Db 269 ----- 269
```


Db 11692 CTGTGACTTCAATGTGAAGTATACGAAGATGATATATTGGAAGACTTTGGGACTTGA 11751
QY 268 -----Gly----- 268
Db 11752 GGGAGAGGCTCATCTGGACATCACGAGCCAGACTGACTGACTTCCATCTGCACTACAA 11811
QY 269 -----Val----- 269
Db 11812 AGAAGACAAGACAAGTGTCTGCTCTGCTCAGACGCTCCCGAGCCATAGGCACTGTGAGTCT 11871
QY 270 -----Lys----- 270
Db 11872 GGATGCAAGCAGACAGATGACCAAGAGTGTGAGGCTGAATGTCTACTTCCGCGCTCAGTCCCC 11931
QY 271 -----ValGlu----- 272
Db 11932 TCCAGATAATAACTCAGCATATTCAAAATGGAGTGGAGGACAAAGGAGCTGTGATGGTGA 11991
QY 273 -----Asn-----Arg---Pro--- 275
Db 11992 AACATACATCAAAATTAACCTGGGAAGAAGACAGCTTTTCAGATTGCTAGACTCCCTAA 12051
QY 276 -----Phe-----Leu---SerLysLeulle--- 281
Db 12052 AAGCAATGTGCCAAGGCTTCTGAGGCTGTTTATGATTATGTCAAGAA---GTACCAGCT 12108
QY 282 -----PhePhe----- 283
Db 12109 GGGACATGCTTCTTTCAGACTAAGAAAAGTCTTCAGATGATGCTGAACAGCCATAAG 12168
QY 283 ----- 283
Db 12169 GATGTTGATGAGATGAACGTGAATGCCAGAGGGTAAACCGTGATACCTACCAGAGTCT 12228
QY 284 -----Asn----- 284
Db 12229 ATATAAGAAGATGTGGCTCAGGAGGCGCAGAGTATCCCTGAGAACTCAAGAAAATGCT 12288
QY 285 Val-----SerGlu-----His-----Asp--- 289
Db 12289 GTTAGGCAGCTCTAGTACGTATTACTCAGAGATGACCATGCGAGTCAACATGGCTGATGA 12348
QY 289 ----- 289
Db 12349 CTCAGTCAATTCATTTCTGAAGTTCATAGAGTCCAGTTCACAGGGAATGCTGGAACATA 12408
QY 290 -----Tyr-----GlyAsn----- 292
Db 12409 TACTGTGACGACACTTTACACTATAGCCATGAGGGAACCAAGAAGTTACTCTCTCAGCT 12468
QY 293 -----Tyr-----Thr-----Cys-----ValAlaSer 298
Db 12469 GTTTAATGGGTAGGACACCTGTTTCTCTATGTTCAAGACCAAGTAGAGAAATCAAGAGT 12528
QY 299 Asn----- 300
Db 12529 AATCAATGACATAACATTAAATGTCCCTTTTCCCAACACCTTGTAACTAAAGATGT 12588
QY 301 -----Leu-----Gly-----His-----Thr----- 304
Db 12589 CCTATTGATTTCAGGGAGGACTTAAACATTTTATCCAACTTAGGCCACAGGATATCAA 12648
QY 304 ----- 304
Db 12649 TTTTACAACAATACTAAGTACTTTTCAGAGCTTTTGGAGAGACTTTTATAGACATCATAGA 12708
QY 304 ----- 304
Db 12709 AGAAAAAATTAATGCCTTAAGACAACAATGAATCTACTTGTGTCCTGTATCATCAACAT 12768
QY 305 -----AsnAla----- 306
Db 12769 GTTCTTCAAAACACATATCCCATTTGCATTTAAATCCCTTGAGAGAAACATATACTCTGT 12828

QY 307 -----SerIleMet----- 309
Db 12829 CTTGAGTGAAGTCAATGACTTTGTTTCAATCCATATCTTCAAGAGGGTCTTATAAGCTACA 12888
QY 310 -----Leu-----Phe----- 311
Db 12889 GCAGGTCCATCAGTATATGAGGCTTTTCGTGAGAGAGTATTTTGATCCGAGTGTGGTGG 12948
QY 312 -----Gly-----Pro--- 313
Db 12949 CTGGACAGTAAATATTATGAATAGAGAAAGATGGTTGACCTTATCAAGACCTTTT 13008
QY 313 ----- 313
Db 13009 GGCTCCTCTGAGGATTTCTACTCTGAATACAGTGTGACAGCTGCTGATTTGTTGTTCCAA 13068
QY 314 -----Gly---Ala-----ValSer----- 317
Db 13069 AATGTCAACTCAGGTTGAGCAATTTGTGCCAGGATATCAGAGAGTATCTTAGCATGCT 13128
QY 318 -----Glu----- 318
Db 13129 TGCTGACATAAATGGAAGGGGAGGAAAAGTTGTCAGAGCTTTCTATTGTGTAAGGA 13188
QY 319 -----Val-----SerAsn----- 321
Db 13189 AAGAATAAAGCTGCTGCTCAGCTGGGTGGCAGAAATAACGTCGTGATTACCTCCGGCAGCT 13248
QY 322 -----Gly----- 322
Db 13249 CCATTCCAACTGACAGGATTTTTCAGACACAGCTCTCTGGCTACTATGAAAAATTCGTTGC 13308
QY 323 -----Thr-----SerArg----- 325
Db 13309 TGAGTCCACAAGACTGATGACTGCTCCATTCATAAACTACACATGTTTCTCAGATACAT 13368
QY 326 Arg-----AlaGly----- 328
Db 13369 CGCTGAGTTACTGAAAAGCTGACAGTGGCCACAGCCCAATATGCGCTGCTGAAAAGGG 13428
QY 329 -----Cys 329
Db 13429 GGATTTTGAAGCTGCTGGAAGTTGGGATCGCCTGCTCTACAATGAAGCTTGTCTGT 13488
QY 330 Val-----Trp-----LeuLeu----- 333
Db 13489 GTCCGACAGGCTTACCGGGAAGTGAATGGCTGAAGGCTCTCGCTTCTTCAGCATGGA 13548
QY 334 -----ProLeu---LeuValLeuHisLeu-----Leu 341
Db 13549 CGAGAGATTGAATATGGTTTCAGACCCCTTTCATCTGCTCTCCATCTGCCACCATGCTT 13608
QY 342 -----LeuLys-----Phe 344
Db 13609 CCGAAAACCTCAGGACTTCGCTGCGCAAGGCTGCTGGGAAGCAGACAGCGGCTTT 13662

RESULT 17

BC038478

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 8259)

REFERENCE

AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Stenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stratton, M., Soares, M.B., Bonaldo, M.F., Casavant, J.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carnanci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketterman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 8259)

Strausberg, R.

Direct Submission

Submitted (04-OCT-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgaps-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NIISC), Gaithersburg, Maryland

Web site: <http://www.nisn.nih.gov/>

Contact: nisc.mgc@nih.gov

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghghi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W., Tsurgion, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

REMARK COMMENT

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 80 Row: j Column: 1

This clone has the following problem: frame shifted.

FEATURES

source

1..8259

Location/Qualifiers

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:422918"

/tissue_type="Kidney, normal. 5 month old male mouse."

/clone_lib="NCI CGAP_Kid14"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

ORIGIN

Alignment Scores:

Pred. No.:	2,55e-13	Length:	8259
Score:	1683.60	Matches:	273
Percent Similarity:	13.36%	Conservative:	53
Best Local Similarity:	11.19%	Mismatches:	10
Query Match:	69.92%	Indels:	2104
DB:	11	Gaps:	238

US-10-017-084A-523 (1-344) x BC038478 (1-8259)

QY	1	Met	-----Lys-----	2
Db	929	ATGTGGAGACCCAGCTGGACACCCAGAGAGGCAAAAGTGTGCTGCCAATAATGACAAGA	988	
QY	3	Thrile	-----Gln-----	5
Db	989	ACCGTACTTCTCTGTCTGTGTATGTCCTGAAAGTGACAGGACTCTAAGGTGACTGTGC	1048	
QY	6	-----Prolys-----Met-----His-----	9	
Db	1049	TCTTTGCTGGCCAAACATATTGCCAAAGAGCCCTTTGAGGTGTATGTGGACAAGTCACAGG	1108	
QY	9	-----	9	
Db	1109	GTGATGCCAGCAAAAGTGAAGTGCCTCCAGGGCCCTGGTCTGGAGCCCAATATTGCCA	1168	
QY	9	-----	9	
Db	1169	ACAAGACTACTTACTTTGAGATCTTCACCTGCAGGAGCTGGCATGGGTGAGGTGGAAGTTG	1228	
QY	10	-----Asn-----Ser-----	11	
Db	1229	TCATCCAGGACCCCTACAGGACAGAAAGGCACAGTGGAACTCGCTGGAGGCCAGGGGTG	1288	
QY	12	-----IleSer-----Tyr-----AlaIle-----	16	
Db	1289	ACAGCACCTATCGCTGTAGCTATCAGCCACCATGGAGGGGTGTCCATACAGTACATGTCA	1348	
QY	17	-----Phe-----	17	
Db	1349	CCTTCGCCGGTGTTCCTATCCCTCGTAGCCCTACACTGTCTACTGTGGCCAGCCTGTA	1408	
QY	18	Thr-----GlyLeu-----Ala-----AlaLeu-----	23	
Db	1409	ACCCAGCTGCTGCGCGGCTATTGGTAGAGGCTTCAGGCCAAGGCTGTTCCAGTAGAGG	1468	
QY	24	-----Cys-----	24	
Db	1469	AAACAGCCGACTTCAGAGTGTACAAAGGGCGCTGGCAGTGGGGAGCTAAAGGTCACTG	1528	
QY	25	-----Leu-----	25	
Db	1529	TAAAGGTCCTCCAGGTGAGGAGCGGTAAAGCAGAGGAGCTTAGGGGAGTGTGTATGCG	1588	
QY	26	Phe-----Gln-----	27	
Db	1589	TTTGAATATTACCTACATCCCTGSCACATACACTGTCCACATCAGTGGGGTGGCCAG	1648	
QY	28	-----Gly-----ValPro-----Val-----	31	
Db	1649	AACATTGGTGAAGTCCGTTTGAGGTGAAGGTAGGCACCTGAGTGTGGCAATCAGAAAGTT	1708	
QY	32	Arg-----Ser-----	33	
Db	1709	CGGGCATGGGTCTCGGCTCGAAGAGGAGGCAATTGTTGGCAAGTCAGACAGCTTCGTAGTA	1768	
QY	34	-----GlyAsp-----AlaThr-----Phe-----Pro-----LysAla-----	41	
Db	1769	GAGGCCATTGGTGAATGATGGGACCTTTGGGTCTCTGTGGAAAGGTCCATCAGACAGCA	1828	
QY	42	Met-----Asp-----	43	
Db	1829	AGATTGATGTGACGACAAAGGGTGTGGCTCTGTGTGCTATTTGGCCCGCCAGGAG	1888	
QY	44	-----Val-----Thr-----	46	
Db	1889	GCTGGCGAGTATGCTTTCATGTGTGTAAACAGTGAAGGATATCGTCTCAGTCTCTTTC	1948	
QY	47	-----ValArg-----Gln-----	49	
Db	1949	ATGGTGTACATCCGTGAGGACACCCAGGATTTTCCACCCAGAGGTTTGAAGCACTGGG	2008	

```
QY 50 ---Gly---Glu---Ser---Ala---Thr---54
D 2009 CCTGGATTGGAGAACTGCTGGTGGCTGTCAACAAGCCAGCAGAGTTTCACAGTTGATGCC 2068
QY 55 ---Leu---Leu---Cys---57
D 2069 AAGCATGCTGGGAAGGCTCTCTTCGAGATTCAAGTTCCAGACAAATGAGGGCTGCTCTGTG 2128
QY 58 ---Thr---Asp---Arg---62
D 2129 GAAGCAGACTCAGGACAAATGGCAATGGTACTTACAGCTGTTCTTATGTGCCAGAAAG 2188
QY 63 ---Val---Thr---ArgValalaTrp---Leu---Asn---70
D 2189 CCAGTGAAGCACACAGCCATGTTTCTTGGGGAGGTGTCCAGCATCCCCCAACAGTCCCTTC 2248
QY 71 Arg---Ser---72
D 2249 CGGTGATGTGGGAGCTGGCAGCCATCCAAACAAAGTCAAGGTGTATGTTCCAGGAGTG 2308
QY 73 ---ThrIleLeu---Tyr---Ala 77
D 2309 GCCAAGACTGGGCTCAAGGCCCATGAACCTACTACTTACTGTGGATTGTACTGAAGCT 2368
QY 78 Gly---78
D 2369 GGCCAGGAGATGTCAGCATTTGGTATCAAGTGTGCCCTGGAGTAGTGGGCCCCCACTGAG 2428
QY 79 ---LysTrp---82
D 2429 GCTGATATTGACTTTGATATCATCGCAATGACATGACACTTCTACTGTAAATACACA 2488
QY 83 ---Cys---Leu---Asp---85
D 2489 CCCTGTGGGGTGGCAGCTATACCATCATGTCCTTTTGTGTGACCCAGGCCACCCACC 2548
QY 86 ---Pro---ArgVal---Val---89
D 2549 AGCCCATCAGAGTCAAAAGTGAGCCTTCTCATGATGCCAGAGGTGAAGGCTGAGGGT 2608
QY 90 ---Leu---Leu---Ser---Asn---93
D 2609 CCTGGCCTAAATCGCACTGGTGTGAACTTGGCAAAACCCACCATTTTCACAGTCAATGCT 2668
QY 94 ---Thr---Gln---95
D 2669 AAAACTGCTGGAAAGCAAGCTGGATGTCCAATTTCTCAGGACTGGCTTAAGGAGATGCA 2728
QY 96 ---Thr---96
D 2729 GTACGGGATGGACATCATTTGACCACCATGATATACCTACACAGTCAAGTACATTCCT 2788
QY 97 ---Gln---Tyr---98
D 2789 GTGCAGCAGGGCCAGTAGTGTCAATGTCACTTATGGAGGAGATCAGATCCCAAGAGT 2848
QY 99 ---Ser---Ile---100
D 2849 CCATTTTCAGTGGAGATATCTCAAGCCCTGGATCTCAGCAAAATCAAGGTGTCTGGCCTT 2908
QY 101 ---Glu---Ile---102
D 2909 GGTGCAAAAGTGGACCTTGGCAAGATCAAGAGTTCAAGTAAAGTCAAAAGGTCAGGT 2968
QY 103 ---Gln---103
D 2969 GGTCAAGGCAAGTAGCATCCAGATTGTGAGTCCCTCAGGTGCAGCGGTACCTCTCAAG 3028
QY 104 ---Asn---104
D 3029 GTAGAGCCAGGCTGGAGCTGACACAGCGGTGTTGTTTGTGCCCCGTGAAGAGGG 3088
QY 105 ---ValAspVal---TyrAsp---109
```

```
D 3089 CCTATGAGGTGAAGTGAACCTATGATGGTGTGCTGTACCTGGCAGTCCCTTTCACATA 3148
QY 109 ---109
D 3149 GAAGCTGTGGCCCCCACCACCAACCCAGCAAGTGAAGCGCTTTGGACAGGGCTACAGGG 3208
QY 109 ---109
D 3209 GGCATGCAGGCTCCCTGCCCGCTTACCATTGATACAAAGGCTGTGCACTGGTGGC 3268
QY 110 ---GluGlyPro---Tyr---113
D 3269 CTGGGCTGACAGTGAAGGCCCTCTGTGAAGCACAGCTTGAGTGCCTAGACACAGGGGAT 3328
QY 114 ---ThrCysSer---ValGlnThr---Asp---121
D 3329 GGTACATGCTCTGTGCTTATGTATCCACTGAGCCTGGGGACTTACAACATCAACATCCT 3388
QY 122 ---His---Pro---123
D 3389 TTTGTGACACCCACATTCCTGGATCCCATTCAGGCCCATGTGGCTCCTTTTGTGAT 3448
QY 124 ---LysThr---Ser---Arg---127
D 3449 GCATCCAAAGTGAAGTGTCTCAGGCCCTGGGCTGGAGCGGCTACTGCTGGTGAAGTAGGG 3508
QY 127 ---127
D 3509 CAGTTCCAAGTGGACTGTTCAAGTGTGGCAGTGTCTGAGTTGAGATTGAGATTGCTCTCT 3568
QY 128 ---Val---His---129
D 3569 GAGCAGGACTGCCAGCTGAAGTATACATTCAAGACCATGGTGTGATGTCACACACACCATTT 3628
QY 130 ---Leu---Ile---131
D 3629 ACCTATATTCTCTCTGCTGGGCTTACACTGTTTACCATTCAAGTATGGGGCCAGCCT 3688
QY 132 Val---GlnVal---Ser---135
D 3689 GTGCCCAACTTCCCAGCAAGCTACAGTGGAACTGCTGTAGATACCTCAGGTGTACAG 3748
QY 136 ---ProLysIle---Val---Glu---140
D 3749 TGCTATGGGCTTGGGATTGAAGGTCAAGGTGTCTTCGAGAGGCAACCACTGAGTTCACT 3808
QY 141 ---Ile---141
D 3809 GTGGATCCCGGGCTCTTACAGACTGGAGGCCACATGTCAAGGCTCGAGTGGCCCAAC 3868
QY 142 ---Ser---142
D 3869 CCCTCAGGCAATCTGACAGATACCTATGTGCAAGACTGTGGGGATGGCACAATACAAAGTG 3928
QY 143 ---Ser---AspIle---145
D 3929 GAATACACTCCATATGAGGAGGAGTACACTCTGTGGATGTGACTTATGATGGCAGCCT 3988
QY 146 ---Ser---146
D 3989 GTGCCAGAGCCCTTCAGGTGCTGTAAACAGAGGGCTGTGACCCCTCCCGGGTGGT 4048
QY 147 ---Ile---Asn---148
D 4049 GTCCATGGAACCGGATCCAAAGTGTGACCAACAAACCAAAAGTTTCACAGTAGAA 4108
QY 149 ---GluGly---150
D 4109 ACCAGGAGCTGGCACAGGTGGCTGGCTTGGCTGTGTGAGGGTCCCTCAGAGGCCAAG 4168
QY 151 ---Asn---151
```


QY 233 Val-----Pro-----Valgly----- 236
Db 6389 GTGAAGAGAGTATACACGAGGCGACGTGCCCTTCTGTGGCCAATATTGGCAGTCAT 6448
QY 237 -----Gln----- 237
Db 6449 TGTGACCTCAGCCTGAAGATTCTGAAATTAGCATCCAAGATATGACAGCCAGGTGACC 6508
QY 238 -----Lys-----Gly-----ThrLeuGln 242
Db 6509 AGCCCATCAGGCAAGACCCATCAGGCGAGAGATCGTAGAAGGAGAGAACCATCTTAC--- 6565
QY 243 Cys-----Glu-----AlaSerAla----- 247
Db 6566 TGTATCCGATTGTGCTCTGAGTGGGAATGCATACAGTCAGTGTCAAGTACAAAGGCG 6625
QY 248 -----ValPro-----SerAlaGluPheGln----- 254
Db 6626 CAGCATGTACCTGGGAGC--CCCTTCCAGTTTCACTGTGGGGCCTCTGGGGGAAGGGGT 6682
QY 254 ----- 254
Db 6683 GGTCAAGGTCGTGTCTGGAGGCCCTGGCCCTAGAGAGGGCTGAAGCTGGAGTGCACGG 6742
QY 255 -----Tyr-----Lys----- 255
Db 6743 GAGTTGGGATTGTGACTAGGGAAGCTGGCGCTGGAGGCTGGCCATCTGCTGTGAAGGC 6802
QY 255 ----- 255
Db 6803 CCCAGCAGGCTCAGATCTCTTCGAGGACCGAAGGATGGCTCCTGTGGTGTGGCTTAC 6862
QY 256 -----Tyr-----Lys----- 257
Db 6863 GTAGTTCCAGAGCCAGGTCAGTATGAGGTCTCAGTCAAGTTCAACAGAGAGCACAATCCT 6922
QY 258 Asp-----Asp-----LysArgLeu-----Ile 263
Db 6923 GATAGCCCTCTGTGGTGGCTGTGGCTTCTCGTCTGGTGACGCGCGGCTTACTGTT 6982
QY 264 -----GluGlyLysLysGlyValLysValGluAsnArgPro-----Phe----- 276
Db 6983 TCTAGTCTTCAGGAG-----TCAGGGTTAAAGTGC--AACCAGCCAGCATCTTTTGA 7033
QY 277 -----Leu-----Ser----- 278
Db 7034 GTCACTCTGAATGGAGCCAGGGGCAATTGATGCCAAGGTGCCACAGCCCTCAGGAGCT 7093
QY 279 -----LysLeu-----Ile-----Phe----- 282
Db 7094 CTGGAGGAGTGTATGTACAGAGATTGACCAAGATAGTATGCTGTGGGTTTTCATCCA 7153
QY 283 -----PheAsn-----Val-----Ser 286
Db 7154 CGAGAGATGGCATCTACTTGTATGATGTCAAGTTTCAATGTGACTCAGATTCCTGGAAGT 7213
QY 287 -----Glu-----His-----Asp----- 289
Db 7214 CCCTTCAAGATCCGAGTTGGGAGGCTGGGCATGGAGGGACCCAGGCTTAGTGTCCGCC 7273
QY 290 TyrGly----- 291
Db 7274 TATGGAGCAGGCTCGAAGGTGGTGTACAGGAGGCCAGCAGAGATTATTGTGAACACA 7333
QY 292 -----Asn-----Tyr-----Thr----- 294
Db 7334 AGCAATGACAGAGAGTGGTGGCCCTTTGGTTTACCATTTGATGGCCCTTCAAGGTGAAGATG 7393
QY 295 -----Cys-----Val-----Ala----- 297
Db 7394 GATTGCCAGGAGTGGCCCGGAGGGCTATCTGTGCACCTATACCCCATGGCACCTGGCAGC 7453
QY 298 -----SerAsnLysLeuGly-----His----- 303

Db 7454 TACCTCATCTCCATCAAGTATGGTGGCCCTTATCATCATTTGGTGAAGTCCCTTTAAAGCC 7513
QY 304 -----Thr-----Asn-----AlaSerIleMet 309
Db 7514 AAGGTCAAGGTCCTCGTCTTGTGAAGCAACACAGCCTCCATGACACATCATCTGTG--- 7570
QY 310 LeuPhe-----GlyPro 313
Db 7571 ---TTTGTGGAATCTTTGACTAAAGTTGCCACGGTTTCCCCAGCATGCAACCTCAGGCCCA 7627
QY 314 Gly---Ala---ValSerGluVal----- 319
Db 7628 GGTCTGTCTGTATGTCAGCAAGTAGTAGCCAAAGCCTGGGCTTAAGCAAGCTTATGTA 7687
QY 320 -----SerAsn----- 321
Db 7688 GGCCAGAGAGCACTTTCACAGTAGATTGCAGCAAGCAGGTAACACATGCTGCTGGTG 7747
QY 322 -----Gly-----Thr-----SerArg 325
Db 7748 GGCCTGCATGGCCCAAGGACACCCCTGTGAAGAGATCCTGTGTAACACATGCGCAGCGC 7807
QY 325 ----- 325
Db 7808 CTCTATAGTGTCTTCTTACCTGCTCAGGACAAAGGGAGTAGACACTGCTGCTCAAGTGG 7867
QY 326 -----Arg-----AlaGlyCys--- 329
Db 7868 GGTGATGAGCATATCCAGGAGCCCATACCGCATATTATGTTACCTGAGCC---TGCCAC 7924
QY 330 Val---Tyr----- 331
Db 7925 CTAAGTTGGACCTGTGCCAGTGAAGCTCCCATGCAATGAGCATCCCAACACCTGTC 7984
QY 332 -----Leu----- 332
Db 7985 CTATTCACAGAGCCCATTTCTTCTTCGTGAGCCCTGGACCCCTCCCTCCCTGGATCA 8044
QY 333 Leu---ProLeu-----Val-----Leu--- 338
Db 8045 CTCCTGGCGCTTCTCACTGCACTTCGCTTGCCTTGCCTGCACTGTGTTTCACTGCTCTGGGC 8104
QY 339 ---HisLeu-----Leu----- 341
Db 8105 TTTCACTTGGCAGAGGAGGCCATTGTGTGAGAGCATGCTCTTTGTTGTTGGGAGG 8164
QY 342 -----LysPhe 344
Db 8165 TGGAGTCTTATGTACAAACCACTTCTAGTTCTCTTTCCAGCCAGAGGATATAAATT 8224
RESULT 13
AY404420 12304 bp DNA linear GSS 15-DEC-2003
LOCUS Mus musculus LRP1 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY404420
VERSION AY404420.1 GI:39760397
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 12304)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
Gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 12304)

AUTHORS

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.

TITLE

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA

JOURNAL

This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

COMMENT

FEATURES

source

1. .12304

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

<1..>12304

/gene="LRPI"

/locus_tag="HMI1884"

gene

ORIGIN

Alignment Scores:

Pred. No.: 1.66e-12 Length: 12304
 Score: 1682.60 Matches: 296
 Percent Similarity: 10.70% Conservative: 35
 Best Local Similarity: 9.57% Mismatches: 7
 Query Match: 69.88% Indels: 2755
 DB: 29 Gaps: 260

US-10-017-084A-523 (1-344) x AY404420 (1-12304)

```

Qy 1 Met-----LysThrIle-----4
Db 630 ATGGACTTCAGTTATGCCAATGAGACTGTATGCTGGGTGCACGTTGGGGCAGTGTGCC 689
Qy 5 ----Gln-----Pro-----Lys-----Methis---9
Db 690 CAGACAGACTCAAGTGTGCCCGATGCTTGGCTGAAGGCTTTGTGGATGAGCATACC 749
Qy 10 ---Asn-----Ser-----IleSerTrp-----14
Db 750 ATCAACATCTCCCTCAGCTGCACACCGTGGAGCAGATGCCATCGACTGGCTGACGGGA 809
Qy 15 -----Ala-----IlePhe-----17
Db 810 AACTTCTACTTTGTGCGACGACATTGACGACAGGATCTTTGTCTGTAAACCGAAACGGGAC 869
Qy 18 -----Thr-----Leu-----GlyLeuAla-----21
Db 870 ACCTGTGTCTCTGTGCTGACCTGGAACTCTACAAACCCCAAGGCATCGCTTGGACCCC 929
Qy 22 Ala-----Leu-----Cys-----24
Db 930 GCCATGGGAAGGTGTTCTTCACTGACTACGGGCAGATCCCAAAGTGGAGCGCTGTGAC 989
Qy 25 -----Leu-----Phe-----26
Db 990 ATGGATGGCAGACACCGCACCAGCTGGTGTAGTAGAAGATCGTGTTCACACGGGCATC 1049
Qy 26 -----26
Db 1050 ACCCTGACCTGGTACCGGCTCGTCTACTGGGCGGAGCGCTACCTAGACTACATCGAG 1109
Qy 27 -----GlnGly-----28
Db 1110 GTGTGTAGTACGAAAGGAAGGGTCGGCAGACCATCATCCAAAGGCATCCTGATCGACAC 1169
Qy 28 -----28
Db 1170 CTGTACGGCTGACCGGTGTTGAGAACTATCTCTACGCCCACTCGGCAATGCCAATGCCAAC 1229
Qy 28 -----28
Db 1230 ACGCAGCAGAGACGAGCGGTGATCCGAGTGAAACCGGTTCAACAGTACTGAGTACCAAGTC 1289

```

```

Qy 29 -----Val-----Pro---30
Db 1290 GTCAACCGGTGTGGAACAAGGTGTGTCCTGCATATCTACCAACGAGCAGCCGACCCGGA 1349
Qy 31 ValArgSer-----Gly-----Asp---35
Db 1350 GTGCGGAGTCAACGCTGTGAGATGACCAAGTACGGGAGCCAGGTGGCTCCGACATC 1409
Qy 36 -----Ala-----Thr-----Phe-----38
Db 1410 TGCTCTCTGCGCAACAGTCAACAGGCAAGGACCTGCAGGTGACGCTGTGGCTTTCAGCCTG 1469
Qy 39 -----Pro-----Lys40
Db 1470 GGAAGTGTATGGGAAGTCTTGTAAAGAAACCTGAACATGAGCTGTTCCTCGTGTATGGCAAG 1529
Qy 41 -----AlaMetAsp-----43
Db 1530 GGCCGACGAGCATCATTAGAGGCATGGACATGGGGGCCCAAGTCCAGATGAGACATG 1589
Qy 44 -----Asn-----44
Db 1590 ATCCCATCGAGAACCTTATGAATCCACGCGCTCTGGACTTCCACGCCGAGACCGGCTTC 1649
Qy 45 Val-----Thr-----Val-----ArgGln-----Gly-----50
Db 1650 ATCTACTTTGCTGACACCAACCACTACCTCATTTGGCGGCCAGAAAATTGATGACCGGAG 1709
Qy 51 ---GluSer-----Ala-----53
Db 1710 AGAGAGACTATCTCGAAGGATGGATCCCAATGTGGAGGGCGTAGCCGTGGAGTGGATG 1769
Qy 54 -----Thr-----Leu55
Db 1770 GGAACAATCTTTACTGACTGATGATGCCCCCAAGAACCACTTAGTGTGGCCAGGCTG 1829
Qy 56 -----Arg-----Cys-----Thr-----58
Db 1830 GAGAAAGCGCTCAGACCCGGAAGACTTAATTGAGGGCAAGATGACACACCCAGGGCC 1889
Qy 59 Ile-----Asp-----Asn-----61
Db 1890 ATTGTAGTGGATCCACTCAATGGTGGATGTCTGACAGACTGGGAGGAGGAGCCCAAG 1949
Qy 62 -----Arg-----62
Db 1950 GACAGTCGGCGAGGGCGGCTCGAGAGGGCTTGGATGSAAGGCTCACACCGAGATATCTTT 2009
Qy 63 ValThr-----Val-----Ala-----67
Db 2010 GTCACTTCCAAAGACAGTGTCTTGGCCCAATGGCTAAGCTGGATATCCAGCGGAGCGC 2069
Qy 68 -----Trp-----68
Db 2070 CTCTACTGGGTGGATGCTTCTATGACCAATTGAGACCATACTGCTCAATGSCACAGAC 2129
Qy 69 -----LeuAsn-----70
Db 2130 CGGAAGATTGTATAGGGTCTCTGAACCTGAATCATGCTTGGCCCTGTGTCAACATGGC 2189
Qy 71 -----ArgSer-----72
Db 2190 AACTACTCTTTTGGACCGAGTACCGGAGCGGCGAGCGTCTACCGCTTGGAAACGGGGCGTG 2249
Qy 73 -----Thr-----Ile74
Db 2250 GCAGGGCACCGCCACTGTGACCTTCTGCGCAGGAGAGACCGCTATCTTTTGATC 2309
Qy 75 ---LeuTyr---Ala-----Gly-----Asn---79
Db 2310 CGAATGTACACCGCAGCAGCAGCAAGTGGGTACCAAAATGCGCGGGTAAATAACGGA 2369
Qy 79 -----79

```

Db 2370 GGCTGCAGCGCTGTGCTGCTGCCACCCCGGGAGCCCGAGTGTGCTGTGCCGAGGAC 2429
QY 80 -----App----- 80
Db 2430 CAGGTGTTGGACACAGATGGTGTACCTGTGCTGGCGAACCCTCCTACGTGCCGCCACCC 2489
QY 81 -----LysTrp----- 82
Db 2490 CAGTCCAGCCGGGGAGTTGGCTGTGTCGCAACACCGCTGCATCCAGGAGCGCTGGAG 2549
QY 83 -----CysLeuAsp----- 85
Db 2550 TGTGACGAGACACAGCTGTCTGCACACAGCGATGAGGCCCGCAGCACTGTGCCATCAA 2609
QY 86 -----Pro-----ArgVal-----Val----- 89
Db 2610 CACACCTGTCTCCGACCGATTCAAGTGTGAGAACAAACCGGTGTATCCCAACCGTGG 2669
QY 90 LeuLeu-----SerAsn-----Thr----- 94
Db 2670 CTCTGTGATGGGATATGATTGTGGCAACAGCGAGGAGGATCCATGGCCACGTGCTCA 2729
QY 95 -----GlnThr-----GlnTyrSer-----IleIleIle----- 102
Db 2730 GCCCGCACCTGTCCACCAACAGTCTCTGTGCGAGTGGCGGATGCATTCCTATCTCA 2789
QY 102 ----- 102
Db 2790 TGGACCTGTGTGATGTGATGACTGTGTGGGACCGGTCCGATGATGATGACCTCATGGGCC 2849
QY 103 -----Gln-----AsnVal 105
Db 2850 TACCCCACTGTCTCCCTGACTCAATTACTGCAACAATGGCAGATGATTAACATC 2909
QY 106 -----Asp----- 106
Db 2910 AACTGGCGGTGTGACAAACGACAATGACTGTGGGACAAACAGCGACGACCGGTGCAGT 2969
QY 107 -----Val----- 107
Db 2970 CACTCTGTCTCAGTACCAGCTTCAAGTGCACAGTGGCAGATGCATCCCGAGCACTGG 3029
QY 108 -----Tyr-----AspGlu----- 110
Db 3030 ACGTGTGATGGGACAAATGATTGTGGGACTACAGCGACGACACACGCCAACTGTACC 3089
QY 111 -----Gly----- 111
Db 3090 AACCAAGGCTACAGACCTCTCTGTGGTGGCTGCCACTCGGATGAGTTCAGTGCCTCCTAGAT 3149
QY 112 -----Pro-----Tyr-----Thr-----Cys----- 115
Db 3150 GGCCTGTGATCCCCCTGAGTGGCGCTGGAGGGGACACCGACTGCATGTATCCAGC 3209
QY 116 -----Ser-----ValGlnThr----- 119
Db 3210 GATGAGAAGAGCTGTGAGGCGTG-----ACCCATGTTGTGACCCGAAATGTCAAGTTTGGC 3266
QY 119 ----- 119
Db 3267 TGCAGGACTCCCGCGGTGCATFACGAAAGGGGTGGTGTGTGATGGGACAGCGACTGT 3326
QY 120 -----AspAsn-----HisPro 123
Db 3327 GAAGATTAATCCGACGAGGAGAACTGTGAGGCCCTGGCCTGACGGCCACCTCCCATCCC 3386
QY 124 -----LysThrSerArgVal----- 128
Db 3387 TGGCCCAACACACCTCT-----GTCTGCTGCTCTCTGACAAAGTGTGCGACGCGAAGGAT 3443
QY 128 ----- 128

Db 3444 GACTGTGAGACGGCTCGGATGAGGGCGAGCTCTGTGACCAAGTGTCTCTGAATAATAGT 3503
QY 129 -----His-----Leu-----IleVal----- 132
Db 3504 GGCTGTAGTACAACACTGCTCGGTGGCCCCCTGGTGAAGGCATCGTGTGCTCTTGGCCCTCTG 3563
QY 132 ----- 132
Db 3564 GGCATGGAGCTGGGCTCTGACAAACCACACCTGCCAGATCCAGAGCTACTGTGCCAAGCAC 3623
QY 133 -----Gln----- 133
Db 3624 CTCAAAATGCAGCAGAAAGTGTGACCAACAAGATTCAGTGTGAAGTCTCTGTGTACGAG 3683
QY 134 -----Val-----Ser-----Pro-----Lys----- 137
Db 3684 GGCTGGGTCTTGGAGCCTGAGGGGAAAGTGGCGGAGTCTGGATCCCTTCAAAACCGTTC 3743
QY 138 IleVal-----GluIle----- 141
Db 3744 ATCATCTTCCAAACCGCACGAGATCAGGCGCATTCACCTTCAACAGGGGAGCTACAGC 3803
QY 142 -----Ser-----Ser----- 143
Db 3804 GTCTAGTGTGCTGGCCTGGCAACACTATTGCCCTGGACTTCCACCTCAGCCAGAGTGCC 3863
QY 144 -----AspIle-----SerIle-----Asn----- 148
Db 3864 CTCTACTGGACCGACGTGTGAGGACAAAGTCTACCGTGGGAAACTCTCTGGACACGGA 3923
QY 149 -----Glu----- 149
Db 3924 GCCCTGACAGCTTTGAGTGGTGTGATTGATTGCTTGGCCACACAGAGGGGCTTGCT 3983
QY 150 -----GlyAsn-----Asn-----Ile----- 153
Db 3994 GTAGATTGGATTGAGGCAACATCTACTGGGTGAGAGCAACTCTGGACCATGCAAGTG 4043
QY 154 -----SerLeu-----Thr-----Cys----- 157
Db 4044 GCCAAGCTGGACGGNAACCTTCCGAACCTCTGTGTGGGGGTGACATTGAGCAACCCGAGG 4103
QY 158 -----IleAla-----Thr----- 160
Db 4104 GCCATGCTCTGGACCCCTCGGATGGGATCTGTGTTGGACAGACTGGGATGCCAGCCTG 4163
QY 161 -----GlyArg----- 162
Db 4164 CCACGAATCGAGGCTGCATGCCATGATGGGGCTGGCCGCCGAACCATCCACGGGAGACA 4223
QY 163 -----Pro----- 163
Db 4224 GSCTCTGGGGGTGGCCCCAACGGGCTCACCTGGATTACTTGGAGAAGCGCATCTCTTGG 4283
QY 163 ----- 163
Db 4284 ATTGATGCTAGTGTAGATGCCATCTATTACGCCGGTATGACGGCTCCGGCCACATGAG 4343
QY 164 -----Glu-----Pro-----Thr----- 166
Db 4344 GTGCTTCGGGACACAGTCTCTGTCAACCCATTTGCCGTGACACTGTACGGTGGGAG 4403
QY 167 Val-----Thr-----TrpArg----- 170
Db 4404 GTGTACTGGACCGACTGGCGAACAATACTGGCTAAGGCCAACAAAGTGGAGCTGGCCAC 4463
QY 170 ----- 170
Db 4464 AACGTACCGTGGTACAGAGGACCAACACCGAGCCCTTCGACCTGCAAGTGTATCACCT 4523
QY 170 ----- 170
Db 4524 TCCCGGACCCCATGGCTCCAAACCCATGTGAGGCCAATGGGGCCCGGGCCCTGTTC 4583

QY 171 His-----Ile-----Ser-----Pro----- 174
DB 4584 CATCTGTGCTCATCACTACAAACCGGACCGTCTCTCGGCTGTCCCACTCATGAAG 4643
QY 175 -----Lys-----Ala----- 176
DB 4644 CTGCACAGGACAAACACACCTGCTATGAGTTTAAAGATTCCTCTGTACGCACTGAC 4703
QY 177 -----Val---Gly-----Phe--- 179
DB 4704 ATGGAGATCCGGGGCTGGACCTGATGCCCGTACTACAAATTATATCATCTCTTCACG 4763
QY 180 -----ValSer-----Glu----- 182
DB 4764 GTGCCGTGATATCGACAATGTACCGGTGTGGACTATGATGCCCGAGAGCGAGATTAC 4823
QY 183 -----Asp-----Glu 184
DB 4824 TGGTCTGATGCGGACTCAAGCCATCAAAAGGCATTATCAACGGCACTGGCGTGGAG 4883
QY 184 -----Tyr----- 185
DB 4944 AATCTGTTTGGACAAGTTACGACCAACCAAGAACAGCAGATTAACTGGTCCCGCTGGAC 5003
QY 186 -----LeuGlu----- 187
DB 5004 GGCTCCTTCAAGAATCGGTGTGTCAGGSCCTGGAGACGCCCAACGGCTGTGCTCCAC 5063
QY 188 -----Ile----- 188
DB 5064 CGCTTCTGTGCAAGCTCTACTGGACTGATGGGCAACATCAGCATGCGCCCAACATGGAT 5123
QY 189 -----Gln-----Gly----- 190
DB 5124 GGGAGCAACCACTCTGCTCTTCTAGTGGCCAGAGGGCCCTGTGGGGTTGGCCATTGAC 5183
QY 191 -----Ile-----Thr-----Arg----- 193
DB 5184 TTCCCTGAGAGCAAACTCTACTGGATCAGCTCTGGGAACCAACAATCAACCGTTGCAAT 5243
QY 194 -----Glu----- 194
DB 5244 CTGGATGGAGCGAGCTGGAGGTCTATCGACACCATGTCGGAGCCAGCTGGGGCAAGGCCACT 5303
QY 195 -----Gln---Ser-----Gly 197
DB 5304 GCCCTGGCCATCATGGGGACAAAGCTGTGGTGGGACAGATCAGGTGTACAGAGATGGGC 5363
QY 198 -----Asp----- 198
DB 5364 ACGTGCAACAAAGCCGCTCTGGGCTCGTGTGCTGGGAACAGTACACACCTGTGGTT 5423
QY 199 -----Tyr-----Glu----- 200
DB 5424 ATGCACATGAAGTGTATGACGAGAGCATCCAGCTAGAGCATGAGGGCAACACCCCTGC 5483
QY 201 -----CysSer----- 202
DB 5484 AGTGTCAACACGAGACTGTTCACAGCTCTGGCTGCCACATCAGAGAGCTCGCTCC 5543
QY 203 -----Ala----- 203
DB 5544 TGTATGTGTACAGCGGTTACAGCCTCCGGAGCGGACAGCAGGSCCTGTGAGGCTGGGC 5603
QY 204 -----Ser-----AsnAsp 206
DB 5604 TCCTTTCTCTGTACTCTGTACATGAGGAAATTCGGGGGATTCCACTAGATCCCAATGAC 5663

QY 207 -----ValAlaAlaproVal----- 211
DB 5664 AAGTCGGATGCCCTGGTC-----CCAGTGTCCGGAACCTTCACTGGCTGTGGATCGAC 5717
QY 212 -----Val----- 212
DB 5718 TTCCATGCCGAAATGACACTATTATTATTTGGTGGATATGGGCCTTAAGCACCATCAGCAGG 5777
QY 213 -----Arg-----ArgValLys 216
DB 5778 GCCAAGCGTGCACAGACATGCGGAGAGGATGTGTGACCAACGATTTGGCCGTGTGGAG 5837
QY 217 -----Val-----Thr----- 218
DB 5838 GGCATCGCGGTGGACTGGATCGCAGGCAACATATATGACGGACGAGGGCTTCGATGTC 5897
QY 219 -----Val-----Asn-----Tyr----- 221
DB 5898 ATCGAGGTTGCCCGCTCAATGGCTCTTTTCTGTTATGTGTCAITTTCCAGGGTCTGGAC 5957
QY 222 -----Pro----- 223
DB 5958 AAGCTCGGGCCATCATGTCCACCCAGAGAAGGGGTACTTGTCTTGGACCGAGTGGGT 6017
QY 224 -----Tyr-----Ile-----Ser-----Glu----- 227
DB 6018 CATTACCCACGATTATGACGGCTCTCGCTTGTATGTCACAGAGAGTGGTGTGTGTTAAT 6077
QY 227 ----- 227
DB 6078 GTCAGCATCAGCTGGCCCAATGGCATCTCAGTAGACTATCAGGGCGGCAAGCTTACTGG 6137
QY 228 -----Ala-----Lys-----Gly----- 230
DB 6138 TGTGATGCTCGGATGGACAGATCGAGCGCATCGACCTGGAAACGGGCGAGAACCGGGAG 6197
QY 230 ----- 230
DB 6198 GTGGTCTGTCCAGCAATAACATGATGATGTTCTCGTGTGCTGTTTGGAGACTTCATC 6257
QY 231 -----Thr-----Gly----- 232
DB 6258 TACTGGATGACAGAACTCAAGCCAAATGGCTTCCATCAAGCGCGGCTGCAAGACAATGCT 6317
QY 233 -----ValPro-----ValGly----- 236
DB 6318 ACAGACTCGTCCCTCTCAGGACAGGCAATGGTGTTCAGCTTAAGACATCAAGGTCTTC 6377
QY 237 -----GlnLysGlyThr----- 240
DB 6378 AACAGGGACAGCAGAGGGTACCAATGTGTGCGGGTAGCAACGCGGGGTGCCAGCAG 6437
QY 241 -----Leu-----Gln-----Cys----- 243
DB 6438 CTCTGCTGTATTCGGGGTGGCGGACAGCGAGCCTGTGCTGTGCCCACGGGATGTGCA 6497
QY 244 Glu-----AlaSer----- 246
DB 6498 GAAGACGGGGCTCATCGGAGAGTACGCTGGCTACTGCTCTACTCAGAGCGGACCATC 6557
QY 247 -----Ala-----Val----- 248
DB 6558 CTCGAAGACATCCACTGTGGGATGAGCGTAACTCAACGACCGCTGAGCCCTTTGAA 6617
QY 249 -----ProSerAlaGlu----- 252
DB 6618 GACCCC-----GAGCACATGAAAAATGTATCGCCCTGGCCCTTTGACTACCGAGAGCG 6671
QY 253 -----Phe----- 253
DB 6672 ACCTCCCGGGACCCCTAACCGCATCTTCTTCACTGATCATCCACTTTGGGAACATCCAG 6731
QY 254 Gln----- 254

Db 6732 CAGATCAATGACGATGGCTCGGCGAGGACCAACCATCGTGGAAATGTGGGCTCTGTGGAA 6791
QY 255 -----Tyr----- 256
Db 6792 GGCCTGGCTATCACCCTGGCTGGGACACACTGTACTGGACAAGCTACACCATCCACC 6851
QY 256 -----Tyr----- 256
Db 6852 ATCAACCGCCACACCGTGGACCGAGCTGCCAGGGGCTTCGAGAGGAGACAGTCATC 6911
QY 257 -----AspAsp----- 259
Db 6912 ACCATGTCGGAGACGACACACCGAGAGCCCTTTGTGCTGGATGAGTGCAGAAANNNNNN 6971
QY 259 ----- 259
Db 6972 NNN 7031
QY 260 -----Lys-----ArgLeuIle 263
Db 7032 NNNNNNNNNNACAAGTTCTGCTCAGAGGCACAGTTTCGAGTGCCAGAACCCGGTGATC 7091
QY 263 ----- 263
Db 7092 TCCAAGCAGTGGCTGTGTGACGGTAGCGATGATTCGGGGATGGCTCCGATGAGGCAGCT 7151
QY 264 -----GluGlyLys----- 266
Db 7152 CACTGTGAAGCAAGACATGTGGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 7211
QY 267 -----Lys-----Gly----- 268
Db 7212 GTCCCTGAGCGCTGTGTGATGGCGACAGGACTGTACCGATGGCGGAGTGAAGT 7271
QY 269 Val----- 269
Db 7272 GTCACTGTGGCTGCTGTACACAGCACCTGTGTATGACCGGTGAGTTTCATGTGCCAGAAC 7331
QY 270 -----Lys-----Val----- 271
Db 7332 CGCTTGTGTATTTCCCAAGCATTTCTGTGTCGACCATGACCGGTGACTGTGCTGATGGCTCT 7391
QY 272 -----Glu-----Asn 273
Db 7392 GATGAATCCCTGAGTGTGAGTACCAACCTCGCGGCCCAATGAATTCGGCTGTGCCAAT 7451
QY 274 -----Arg----- 274
Db 7452 GGGCGTTGTCTGAGCTCCGTCAGTGGGAATGTGATGGGAGATGACTGTCAAGACCAC 7511
QY 275 -----Pro----- 275
Db 7512 AGCGATGAGGCTCCCAAGAACCCACACTGCACACGCCAGAGCAAAATGCCATCCTCA 7571
QY 276 -----Phe----- 276
Db 7572 TCACAGTTCTGTGCAGCAGCGGCGCTGCTGGTGGCTGAGGCGTTGCTCTGCAACGCCAG 7631
QY 277 -----LeuSer----- 278
Db 7632 GACGACTGTGGGACCGTTTCAGACGAAACCGGGTGCCATGTCAAGAGTGTCTCAGCGGC 7691
QY 279 LysLeu-----Ile-----Phe----- 282
Db 7692 AAGCTCAGTGGCTGAGTCAGGACTGCGAGGACCTCAAGATAGGCTTTAAGTGCCGCTGT 7751
QY 283 -----Phe----- 283
Db 7752 CGCCCGGGCTTCGGCTTAAGGACGATGCGAGGACCTGTGCCGACCTGGATGATGTCAGC 7811
QY 284 -----AsnVal-----Ser----- 286
Db 286 ----- 286

Db 7812 ACCACCTTCCCTGCGAGCCAGCTCTGCATCAACACCCACGGAAGTTACAAGTCTCTGTGT 7871
QY 287 -----Glu-----His-----Asp----- 289
Db 7872 GTGAGGGCTATGACCCCGTGGCGGTGACCCACAGCTGCTCAAGCTGTGACCGATGAG 7931
QY 290 -----Tyr-----Gly----- 291
Db 7932 GAGCAATTTCTCATCTTTTTCGAAACCGGTACTACTCGGGAAGCTCAACCTGGACGGCTCC 7991
QY 292 AsnTyrThr----- 294
Db 7992 AACTACACACTGTCTTAAGCAGGGCCTGAAACAATGGGTGCTCGCTTGGACTTTGACTACCGA 8051
QY 294 ----- 294
Db 8052 GAGCAGATGATCTACTGCGAGCGTGAACCCAGGGCAGCATGATTGCGAGGATGCAC 8111
QY 294 ----- 294
Db 8112 CTCACCGCAGCAACGTGCTGAGTTCTGCACCGGACGGGCTTAGTAACCCAGATGGGCTG 8171
QY 295 -----Cys----- 295
Db 8172 GCTGTGACTGGGTGGCAACCTGTACTGTGTGTCACAAGGCGCAGAGATACCATGAG 8231
QY 296 Val-----Ala-----Ser----- 298
Db 8232 GTGTCCAAGCTTAACGGGGCTATTCGACACAGTGTGTGCTCAGCTCTGGCTCCGGAGCCCC 8291
QY 299 -----Asn----- 299
Db 8292 AGAGCTCTGTAGTGGATGTACAGATGGGTACTGTGTCGACAGACTGGGTGACCAAC 8351
QY 300 -----Lys 300
Db 8352 TCACTGATCGGCCGGAATTGGCATGGATCTGGCGCAGCATCATCGTGGACACATAAG 8411
QY 300 ----- 300
Db 8412 ATCATATGGCCCAATGGCTGACCGTGGACTACGTACCGAAACGATCTACTGGGCTGAC 8471
QY 301 -----Leu-----Gly----- 302
Db 8472 GCCCGTGGAGTACATTTGAGTTGCGCAGCTGATGGCTCCAACCGTCAAGTTGTGTG 8531
QY 303 -----His----- 303
Db 8532 AGCCAAGACATCCCAACACATCTTTGCGTGCACCTATTTGAAGACTACGTCTACTGGACA 8591
QY 304 -----Thr-----Asn-----Ala-----Ser----- 307
Db 8592 GACTGGGAACCAAGTCCATCAACCGGCCCAAGACACCGGTGCGCAACAAACACTC 8651
QY 308 -----Ile-----Met-----Leu-----Phe----- 311
Db 8652 CTCATCAGACCTGCTGCACCGGCCCATGACATTAATGTTATTCACCGCTTGCACAGCCA 8711
QY 312 -----Gly----- 312
Db 8712 GATGTGCCAATCAACCGCTGCAAGTCAACAAATGGTGTGTCGACCAACCTGTGCTGTG 8771
QY 313 -----ProGly-----Ala----- 315
Db 8772 TCCCTGGGGGTGTGTCATAAATGCGCTGCCCAACCACTTCTATCTATCTGGGTGGCGATGGC 8831
QY 316 -----ValSer----- 317
Db 8832 CGTACTGTGTGTCCAACTGCACAGACAGCCAGTTTGTGTGCAAAATGACAAAGTGCATC 8891
QY 317 ----- 317
Db 8892 CCCCAGATTCAAGTGGCGCCCGCCAGTTCAGTGTCCACCGGCATCTGCACCAACACC 8951

```

Qy 318 -----Glu-----Val----- 319
Db 8952 CTGCTTCATCTGTGATGGGACAAATGACTGCCAAGACATAGTGACAGGCCAATGCG 9011
Qy 320 -----Ser-----Asn----- 321
Db 9012 ACATTACGCTGCTGTGCGCAGCAATTCAGTGCACCAACCAACCGCTGCATTCCTG 9071
Qy 322 -----GlyThr----- 323
Db 9072 GCATCTCCGTTGCAATGGGAGGACAACTGCGGGGACGGGAGGATGACGGGATGCC 9131
Qy 324 -----Se 324
Db 9132 CTGAGGTGACCTGGCGCCCAACCAAGTTCAGTCTCCATCACCAAGCGTGATCCCTC 9191
Qy 324 rArg----- 325
Db 9192 GCGTCTGGTCTGTGACAGGGAATAAGTCTGTGTGGAGCGGAGTGATGAGCGCTGCCAAT 9251
Qy 325 ----- 325
Db 9252 GTACCCAAATGACCTGTGGAGTGATGAGTTCGCTGCAAGGATTCGGCGGTGCATCC 9311
Qy 326 -ArgAla-----G1 328
Db 9312 CCGCGCGCTGGAAGTGTGACGAGAAGATGACTGTGGGGATGGTTTCAGATGAGCCCAAGG 9371
Qy 328 Y----- 328
Db 9372 AAGAGTGTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 9431
Qy 328 ----- 328
Db 9432 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 9491
Qy 329 -----Cys----- 329
Db 9492 NNNNNNCACTCGCGCCCTGCTCTGAGAGTGAGTTTCTCTGCAATGCGCGGTGCATCG 9551
Qy 330 -----Val-----Leu-----Le 333
Db 9552 CTGGCGCTGGAAGTGTGATGGGAGCAACATGACTGTGCGGAGCGGTTCAGACGAGAAAGACT 9611
Qy 333 u-----ProLeu-----Val-----LeuHis----- 339
Db 9612 GCACCCCGCTGTGATGGACCAAGTTCAGTGCAGAGTGCGCACTGCATCCCCCTGC 9671
Qy 339 ----- 339
Db 9672 GCTGGCGCTGTGACCGGATGCTGACTGTATGGACGCGAGTGACGAGGAGCGCTGTGGCA 9731
Qy 340 -----Leu-----Leu----- 341
Db 9732 CTGGGTGAGGACCTGCCAATGGATGAGTTTCAATGTAACAACACTTGTGCAAGCCGC 9791
Qy 342 -----LeuLeu----- 343
Db 9792 TGGCTTGAAGTGTGATGGAGAGGACGACTGTGGGACAACTCAGATGAGAACCCCGAGG 9851
Qy 344 -----Phe 344
Db 9852 AATGCGCGCGTTTCATCTGCCCTCCCAACCGGCTTT 9888

RESULT 19
AY318958/c
LOCUS AY318958 14278 bp mRNA linear HTC 15-JUL-2003
DEFINITION Rattus norvegicus Aal064 mRNA, complete cds.
ACCESSION AY318958
VERSION AY318958.1 GI:32492561
KEYWORDS HTC.
SOURCE Rattus norvegicus (Norway rat)

```

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE

AUTHORS

1 (bases 1 to 14278)

Xu, C. S., Li, W. Q., Li, Y. C., Wang, G. P., Chai, L. Q., Yuan, J. Y., Yang, K. J., Yan, H. M., Chang, C. F., Zhao, L. F., Ma, H., Wang, L., Wang, S. F., Han, H. P., Shi, J. B., Rahman, S., Wang, Q. N. and Zhang, J. B.

Liver regeneration after PH

Unpublished

JOURNAL

REFERENCE

2 (bases 1 to 14278)

Xu, C. S., Li, W. Q., Li, Y. C., Wang, G. P., Chai, L. Q., Yuan, J. Y., Yang, K. J., Yan, H. M., Chang, C. F., Zhao, L. F., Ma, H., Wang, L., Wang, S. F., Han, H. P., Shi, J. B., Rahman, S., Wang, Q. N. and Zhang, J. B.

Direct Submission

Submitted (09-JUN-2003)

Henan Bioengineering Key Lab, Henan Normal University, No. 148 Jianshe Road, Xinxiang City, Henan 453002, P. R. China

FEATURES

source

1. 14278

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

41. 14272

/notes="liver regeneration-related protein LRRG003"

/codon_start=1

/product="Aal064"

/protein_id="AAP85369.1"

/db_xref="GI:32492562"

/translation="MGQPQALRALPLLLFLLLDFTSVAAOATPFKHLKVVSYVE
AESSSGVRGTADRSATKINKEVLEVPQVCTLMRTSOCTKEVTFNPEGLMKK
TKNSGEFASAMRYELKAFPEGKRVALYPMIDGEPNYILNIRGILISALVPPETED
KQVLFDITYGNCSTQVTVNSRGTVATEMSTERNLOHCDGQFQISTISVSLALIKGL
VPLSTLSSQSCQITLEPKRKHVEAICNEQHLFLPFSYKNKGMTHVTKQKLE
DTPKINSRFRFGINGVGLAFESTKSTPPQADAVLKTELKLSISEQNAQRANL
FKHLVTELGLSEATISLLPOLIEVSSPTLQALICQCPQCYTHILOAKTEKAP
LLIDIVYLMALIPNPSVORLOEIAFTELQSRATLYALSHAVNSYAIMDRSPV
LEDIAGLMQIDNECMGDEDFELIRVIGMGTMRVMPALSSVLCNRSPTKPS
LQIQKALQAKRMGMBEVRITLFDTFVNDVAPVEKRLAAYLLMRSPSSDINKIA
KLQWQSQVNFVASHIANILNISEELVQDLKNLKNALVNSRLPTIMDFKFRFN
YQISKSVALPDPVPSATKGNLVPFDSYLPKESMLKTLTVFGIASLDLEIGLEG
KGFEPTLEALFGKQGFPPDSVNKALYVWNGVDPKSVLVDHFGTKDDKHEQDMVN
GIMPIVDIKELIKKEIPEARAYRILKGLGFLVRLOLVGLKLLANGAOTFRGVP
QMTVQAIRGSKDILFLHYFMENAFELPTVGLOLOVSSSGVPTGICAGVLELAN
IOAEVAKPSVSELEFVFMGILIDPEAKSGVQMTNPFHESGLEARVALKAGLQYII
PQKRPVKLPSGNTLHLVSTTKTEVPELLENKRSWSTCKEFTFGMNTCTTGAYNA
STESASVYPLTDTRYLELELKTGEVQYSASATYELLKEDSLVDTLKFLVQAEV
QOSEATAMFKYRERTLSSEVLIPGDFNFGTILRVNDESSKDKNTYKLLIDIQNK
ITEVSVGVHSYDKKDGKGVWSIPRIQAEARSEVTHWSPTKLLFQWSSATAYG
SITSKRWAWRYDNEKIEPDWNTGTNVDTKKVASNFPVDLSRYPRMVHVEANGILDHRI
POTDMTFHMGSKLVDHLNGISELNLKPKVLPDPhiPDLPLKTDGRVKYTLNKR
EIDILPLGKSKSKLVPESVRTPALNPKSVGFHLPSEVQIPFTIIPKTLQQLVPL
LGILDLSTNVLYNWSVYTGNTSRDHFSLQAYRMKADSVDLFSYVQSGSET
TYDSKSTFTLSLDCSLHHKFLDSKFVKHVEFGNNPVSGLLTFTETSAFGQMSAT
VQDQKKKQHLVYDIDKQDQRFVSLYAQGYGLSYERSDMSGTQMSGSNNKFNSTY
FOGTNOIVGMYQDGLSVTSDLOGIPKNTASLKYENYELTKSDSGQVFNPAAS
SLTKAQDQVSTSATNLKYSPILLLENELNSELGLSGASKMLSTSGRFEKHKAFSLD
GRAALTFSGISYQAMILGADSKNVNFKLSREGGLKSNMWMGSKMLGHTHSLR
ISGLSLDNVGNFKGTYQNNELKHITYISYDLVASYRADTVATVQGVFESHRLNRIE
GLASSVDVTTYSYSDPLPNNVFPVLPFTLGVDTHTSGDKMSLWGSHTGQMTSKF
LLKARPLATFSDHYKGSTSHNLVKNYSVSTALEHTLSALTPAOSTSWKEKTSIND
KTYSQEPFANVTMDKIGIELSCRADLSGLYSPIKVPFFYSEFVNLINSLINDADEP
REFTIDAVVKDKNQDHTTISLIPFQSLPDLERNRRTISLLEAMKGLQLSLVDQF
VRKYVALSRPLPQQHLYNLDSDWERQVAGKEKLTDMENYITNDVILALDSAKI
NINELKSLEYAIDQVYRDNYDAQLKRTIAQIDRIIEKLKMLDQIHNIRVLA
KSHNLVLYFENVVDNQISSGASWQNVDTKYQIRIOIEKLMLDQIHNIRVLA
AAELKQOIEALDPMHLPQLRTAILFORISVILIERVKYFVWNLIEDFKVTEKINFRV
IVRELIEKYEVDVQIQVLMDSKIELAHRIYSLSEPLQKSNLVQQIIEIKDYDKVGFPI
DDTVEWIKAVSFNIIIEELNRLIDMSVKLKAFTDYHQFVDKTNKIREMTORINAEIQ
ALELPQKTEALKLWVEDKPTVNSLEKLDKTKVTVDVWLDQDLAQIKAOQDVALED
VADRIYQMDIQGELERCLSLVSQVSYTVVTYISDWMTLTAKNITDKITFAEQYSTQKWAES

VKALVEQGFVPIVEIOTELGTWPAPEVSLHALQEANFOTPDFIVPLTDLRIPSINWEX
MLKNVKIPLRESTPEFTLNTFRVRSFTIDILLEIKAKIIRITDQMSSELOWPLPEVY
LRDLKMNVLISRLKISPLDFHVPETITPEFTIPNVNKLQDLPDLPHPQPHUSCTT
IIPAFKQHLNVLKISPLDFHVPETITPEFTIPNVNKLQDLPDLPHPQPHUSCTT
QAQOQFVLKNNQFTLDSQYKFKLSPVRLDSSKASLANNEIKTLLEAGHMAWTS
VEFNNGIIVKNNQFTLDSQYKFKLSPVRLDSSKASLANNEIKTLLEAGHMAWTS
GTGSMWACPNPDSGDIHSSKISFTVDGPFIASFGLSNNINGKHLRVVOKLTSESQFLN
YSRFEVSKVSHQVSGSILTAEGRALLGDAKEMTGEHNNANLAKVKVLTLSLFLS
AQPELITASTNEGNLKVSPFLKLTGKIDFLNNYALPLSPAQAQSMQSLTRFNQYKI
NONFSAIINNEHMEASIVANGDANLDFINLPUTIPEINLPTFTPLDQFSLWEET
FLWGHNNHNLQFVSDFTGKQTCRATLELSPMTSTILLQVHVSQPSPLDHLHFQDE
WILKASTRELQIDGKROVLOASTSLHYTKNPNGLYLLSPVQELTDREIIPGLKLNDF
PAGKSTRELQIDGKROVLOASTSLHYTKNPNGLYLLSPVQELTDREIIPGLKLNDF
SGIKTYKLKSPPLNLTMLPKVPGVDLTLTOYKPEGSSVPTFTTIPETIOLTVS
OFTLPKSPVGNVFDLNLKLTNLADVLPSLTPEQIEIPLSPLESPVAGFIFFPFG
ELTAHVGNASPLVNTWGTGKADHVEHFDLSTLQFLFETALKVGVGTHRIEND
KFTYIKGTGLQCDNFVKNEDGIFEGLDWLEGEAHLDTSPALDPLHLYKEDKTSV
SASAAIPAIGTVSLDASTDQSVRLNVYFRPQSPDNKLSIFKMEWRKESDGETYIK
INWEBAARFLDLSKSNVPKASEAVDYVKKYHLGHASSELKSLQNDHAETRMVD
EMVNAQVTRDTQSLYKMLAQSQSIPEKLLKMWLSLVRITOKYHMAVTMLMDS
VHFLKFNKRVOPPGNAGTVDELYTIAMRETLLKLSOLENGLHLSFVYDQVEKSR
VINDITFKCPSPCKLKVLLIFREDNLNLSLQGDQINFTILLDSFQFLERLLD
LIEBEKLNKNESTCVDPHNFMTTIPAFKSLRENTISVSEFNDVFOSLIQEG
SYLQOQHOYKMAFEEDVPSVGVMTVYKVEIEKMKVDLIXTLAPLDRKYSVST
AADFASQSTVOEVRSDIREYLSMLADINGKREKVAELISVVKERIDKSWATAVE
ITSDYLRQLHSLKLOPQSLQSGYKFAESTRLDLSIQNYHMFRLYIAELLKQLOV
ATANNGLKGFDEFAVGLQIACLVNGLSVSDEAYAEVNGLKASRFSMBERLNMS
DEFWLSICPCPKRLRDPAGKQWEAPALAKDCAGSQSLGLEKASRSEVQQLFOA
SOAVNKOQIFQVQKSLSDTRVILGLWELVEAPMKDFTSLCHLHTEVCVGRYLRQKV
PRYKQOLIGAMCIVCTWFIKSLITIREAVRLTDNTYKDLVRVREIISALEGKI
RIPTVVDYKEVILLTVPTPTPTQYLCFSLCELTLVSVYTPAHLASAALLARLMHQTO
P"

ORIGIN

Alignment Scores:

Pred. No.: 3 81e-12 Length: 14278
Score: 1679.30 Matches: 283
Percent Similarity: 11.44% Conservative: 45
Best Local Similarity: 9.87% Mismatches: 13
Query Match: 69.74% Indels: 2527
DB: 11 Gaps: 239

US-10-017-084A-523 (1-344) x AY318958 (1-14278)

QY	1	Met	-----Lys-----Thr-----	-----	3
DB	13987	CTCTTTGCTGATGAACCGGTACAGTACCATGACGAGCAATGCCAGAGCTGGAGCTT	13928		
QY	4	Ile	-----Gln-----Pro-----	-----Lys 7	
DB	13927	GTATCTGGGACAGTTTCTCTGCAAGTACCGGCTCACACTCCACTGTCAGGTGAAG	13868		
QY	8		-----Methis-----	-----Asn-----10	
DB	13867	ACACAGGCTTGTAAGTCTTTCATCGGGCAACTTCCACCAACGACCGGATTAGAATGTA	13808		
QY	10		-----	-----10	
DB	13807	CCTCAGGTGTCACTGAGCCCTTCTGACAGAGAATACTGCTGCTTGTTCGCGCCTG	13748		
QY	10		-----	-----10	
DB	13747	GGAGGCTGGAAGAGCTGACAGCCGACTCACTGAAGGCTTCCCTTCTAGTCCAAGCTG	13688		
QY	11	Ser	-----Ile-----	-----Ser 13	

DB	13687	GCTTCCACCTGCACAGTCTTTTGGCCAAAGCGGCTGTCTTCCAGCAGCCTTTGCCAGC	13628		
QY	14	-----Tyr-----	-----14		
DB	13627	GAACTCCCTGAGTTTCCGGAAGCATGTGTGGCAGATGGAGAGCCAGATGAAGGGGTCTGA	13568		
QY	15	-----AlaIle-----Phe 17			
DB	13567	ACCATATTCATCTCTGCTCCATCTGTGAAGAGCGAGAGGCTTTCAGGCCCTTCACTTC	13508		
QY	18	-----ThrGlyLeu-----Ala-----Leu 23			
DB	13507	CGCGTAGGCTCGTCCGACACAGACAAGCCCTTCATTGTAGAGCGCAGGATCCCAACTT	13448		
QY	24	-----Cys-----	-----24		
DB	13447	CACAGCAGCTTCAAAATCCCCCTTTTCAGCAGCCCATTAATTGGCTGTGGCCACCTGCAG	13388		
QY	25	LeuPheGln-----	-----27		
DB	13387	CTTTTTCAGTAACCTCAGCGATGTATCTGCAGAAACATGTGGTAGTTTGAATGGACAGT	13328		
QY	28	-----Gly-----Val-----	-----29		
DB	13327	AATCAGTCTTGTGACTCAGCAAGAAATTTTTCATAGTAGCCAGAGAGCTGGTCTGAAA	13268		
QY	30	-----Pro-----Val-----ArgSer 33			
DB	13267	ATCCTGCAGTTTGAATGGAGCTGCCGAGGTAAATCAGACGTTATTTCTGCCACCGCAGT	13208		
QY	34	GlyAspAla-----ThrPhe-----Pro 39			
DB	13207	GGACAGCTTTTATCTTCTTCTTACCACAATAGAAGCTCTGCAACCTTTTCCCTCCC	13148		
QY	40	-----Lys-----AlaMet-----Asp-----43			
DB	13147	CTTTCCATTTATGTACGACGATGCTAAGATACTCTCTGATATCCCTGGACACAAATTG	13088		
QY	44	-----Asn-----Val-----ThrVal-----47			
DB	13087	CTCAACCTGAGTGCATATTTGGGAAGCAAAATAGCAGCTCTCAGCTGTATTCAGAGTA	13028		
QY	48	-----Arg-----Gln-----GluSerAlaThr-----Leu-----55			
DB	13027	GAAATCCCTCAGAGGAGGCAAGGGTCTTGATAAGGTCAACCATCTTTCTTCTATTTC	12968		
QY	56	-----ArgCys-----Thr-----58			
DB	12967	ATAATATTTTACTGTCCAGCCACCAACACACTCGGATCAAAATACCTCTTACGAAAGGCTT	12908		
QY	59	-----Ile-----Asp-----AsnArg 62			
DB	12907	CATATCTGATGGACCTGCTAGCTTATAGGACCCCTCTTGAAGTAGTGGATTGAACAA	12848		
QY	63	Val-----Thr-----ArgVal-----AlaTyr 68			
DB	12847	GTCATTGAACCTCACTGAAGACAGAGTATATGTTTCTCTCAGGATTTAAATGCAATGG	12788		
QY	69	-----Leu 69			
DB	12787	GATATGTTTGAAGAACATGTTGATATGATAGGAGCACAGTAGATTCAATTGTTCTT	12728		
QY	70	-----Asn-----ArgSer-----72			
DB	12727	TAGGCAATTCATTTTCTTCTATGATGCTCTAAAGTCTCTCCAAAAGCTCTGAAAGTC	12668		
QY	73	Thr-----IleLeuTyrAla-----Gly-----78			
DB	12667	ACTTAGTATTGTTGTAATAATGATACTCTGTTGGCTAAAGTTGGATAAAATGTTTAAGTC	12608		
QY	79	-----Asn-----Asp-----Lys-----Tyr-----82			
DB	12607	CTCCCTGAAATCAATAGGACATCTTTTAGTTTCAAGGTTGTGGGAAAAGGACATTT	12548		

Db 10390 AGTGAGACTTTCTAAGCTGAACTTGTGATCAACACCTCTTTTGGCTGCAGAGTGAGCTT 10331
|||
QY 149 -----Glu-----
|||
Db 10330 TGAGGAATTTGAAGTCATAGTTTGTAGTTCAATGAGGATGAGACAGTGGGCTTTGACTTGGT 10271
|||
QY 151 -----Asn-----
|||
Db 10270 GTTTCGGTTAAGTTCTGCTTGAAGTTCAATGTGAAATTTGGAGCGTGGAGGTTGGCAGT 10211
|||
QY 152 -----Asn-----
|||
Db 10210 TGTTTTCACTGAAGCTTCCATGTTTTCTTTGTTAAGCTAATGTTGCTGCTCATGACTTCC 10151
|||
QY 153 -----Leu-----
|||
Db 10150 CTTTAAAAATTTGTAGTTAGAGACACGCGTGGCTAACTTCAATACTTTTTTCCGCAT 10091
|||
QY 156 ---Thr---Cys-----
|||
Db 10090 CAGACGTGATGTACCTCTAGTTTGTACTGCAGGCGATCCGTGACAAATGAAGAGAAGA 10031
|||
QY 159 ---AlaThr-----
|||
Db 10030 AAGAAAAACGAGCAACGAGATCTGATTTGTATATAAGTCAGCATTTGGTATTCAGTGTGAT 9971
|||
QY 162 -----Arg-----
|||
Db 9970 GACACTTGATTTAAAGAAAAGTCACTAGGTGAAATTTGCCATGGCTGGAATATAAATATT 9911
|||
QY 163 -----Pro-----
|||
Db 9910 GTCAATAGTGTAAATTTCTTGAATCTGGAGGAAACTTGAATAGAGTCTTAGGGAT 9851
|||
QY 164 ---Glu-----
|||
Db 9850 ATGGAATCTGCAACTGTAGAGCGCAGCACTAACCTGTATGAAGGCACAAATGATTT 9791
|||
QY 168 ---Thr-----
|||
Db 9790 AGGACCTGGAATGTGACGCTGGGTGGGATTTGCTTCCGGATCAACATGGCTGGAAGC 9731
|||
QY 169 -----TrpArgHis-----
|||
Db 9730 CAGTGTCTACAGCAAAATGGAGACACTTCAATGTGTGAAGACTGGGATAGTGTGCCAG 9671
|||
QY 174 -----Pro---LysAlaVal---Gly---Phe-----
|||
Db 9670 ATTTGAAAGGCTCTGGAAGGCTGATTTGAGGAAATTTTCAGTTTGTACTTATCAAACTT 9611
|||
QY 180 -----ValSer-----
|||
Db 9610 AATTTTGTTCATATAGTACGCTGAAGAAATGTAATGATGATGCTCTGCTGACTTCTC 9551
|||
QY 182 Glu-----
|||
Db 9550 AAAATTTCTGTCCCAAGAAATGACATTTGTGACATAAATCATAAACATTTTCAGAGG 9491
|||
QY 185 -----Tyr-----
|||
Db 9490 GATAACAACAGAAATGCTGTCTCTGTTCTTTTATATGAGCCTTTTATCTCAAGTCAA 9431
|||
QY 186 -----Leu-----
|||
Db 9430 TGACTGCTTTGTGTCTTCAAAAATTTCTTCAAGCCGTTTCTTCCCATATGAGGAATC 9371
|||
QY 189 ---Gln---Gly-----
|||
Db 9370 CTTCAAGAGGAGTTGTGAACCTTGTGTAAGTAGATTAATTTTCAAGAAATTTTAAAGG 9311
|||
QY 194 -----Glu---Gln-----Ser-----
|||

Db 9310 TATGTTTAAAGAAATCAAGGTTGGCATCTCCATTCATTACTATATATGGCTTCCATGTTGTG 9251
|||
QY 198 -----AspTyr-----
|||
Db 9250 CTCATTGTTTATAGCCGAAAAATTTTGTATGTTTGTACTGATTGAATCTAGTACTCAA 9191
|||
QY 201 -----Cys-----
|||
Db 9190 TTGCAGCTTCTGTTGGGCTGGGGCTCAGAAACAGTGCATAGTTATTTAGGAAGTC 9131
|||
QY 202 -----SerAla-----SerAsnAspValAlaIlePro---ValVal--- 212
|||
Db 9130 TATTTTCCAGCTCAACTTTAGTGAAAACTAAC---TTTCAAAATTCCTTCAATTTTGT 9074
|||
QY 213 -----Arg-----ArgVal-----Lys----- 216
|||
Db 9073 GGATGCAGTAATCTAAATGTTGTGCGAAAGAAAGAAAGATTTTTCACAGTTTCCAAT 9014
|||
QY 217 -----Val----- 217
|||
Db 9013 AACTTTTCCATTAAAGTTGGCAATTTGTCTCACCAGTCATTTCTGCCTTTGCATCCCCAAG 8954
|||
QY 218 -----Thr-----Val----- 219
|||
Db 8953 CAGTCCCGACCTCGGCAGTTAGAATCTGGAGCCACCGTCTGAGATTCAACTTTTGA 8894
|||
QY 220 ---AsnTyr---Pro----- 222
|||
Db 8893 CTCACCTTCAAACTTAGAATAGTTGAGAACCCAGATTGAGAGTCAGTTTTCGGACAAC 8834
|||
QY 223 Pro---Tyr---Ile-----Ser----- 226
|||
Db 8833 CCTTAGGTGTTGGCAATTTATGTTATTGGACAATCCAAAAGAACAAATGGGCCATCCAC 8774
|||
QY 227 ---GluAla-----Lys---GlyThrGly---Val 233
|||
Db 8773 AATGAAGCTAATTTTGGATGATGTATGCTTCTATGAGAAGTTGGAGACAGGCCAGTT 8714
|||
QY 234 Pro----- 234
|||
Db 8713 CCATGACCTGTCTCTGAGAAAGTCCATGTCATATGTCCAGCTTCTAATAGTGTCTTAT 8654
|||
QY 235 -----Val-----Gly-----Gln----- 237
|||
Db 8653 TTCATTGTTGAGAGAAGCTTTACTGGAGAAGTCCAGCCTGGGGACACTCAACTTTGTGAA 8594
|||
QY 237 ----- 237
|||
Db 8593 GTACTTTGTTGACTGTCAAGGTAATTGATTTTATCTTGTGACAACAATACCATTAAT 8534
|||
QY 238 -----Lys 238
|||
Db 8533 AAACCTCACTGATTTTCTCTGTGTGTAATCTTGCACACCGTGTGATTTTCCCTCAAG 8474
|||
QY 239 Gly-----Thr----- 240
|||
Db 8473 GGCCTTTCCAGAACTAATATCTTACCCTCATGCTCCATTTCTCATGTTTACTGTGAGAA 8414
|||
QY 241 -----LeuGln----- 242
|||
Db 8413 GTTCAGGAATTCCTTCAGTACCAGAGGATTAGCATTTTAACCTCCAGAACTGAGCTTGTGC 8354
|||
QY 242 ----- 242
|||
Db 8353 TTGAAAATCAAAATGAGAGCTTCAAATTTGGACTCTCTCTGCGAGTGCAGAGAAGCCAC 8294
|||
QY 243 ---Cys----- 243
|||
Db 8293 AATCTGCTTTGTTCTCTGGAAGTAGTTATGTTCTGTATGTTGGCACTAGCATCTAATAT 8234
|||
QY 244 ---Glu-----Ala-----Ser 246
|||
Db 8233 AAAGAGGGAGATTGGATTTTCAGGACGCTATGATGTTTGCAGAAAGCAGGATTTTCAGT 8174
|||

QY 247 ---Ala--- 247
Db 8173 TGTGCATGAGAGGTGAGAGCTGGAAATCTGTGTATGTGAAGATCAGGAACCTGTAAATC 8114
QY 247 --- 247
Db 8113 TTTGAGATTGACATTTGGGATTGTGAATTTCTGGAATTTGTGATTTCTGGTATACATGAAGTC 8054
QY 248 ---Val--- 248
Db 8053 TGGCAGAGAGAGCTTTGCAAGAGAAATGTTTCAACATCTCCAGGTCTCTCAAATACACTTC 7994
QY 249 ---Pro---SerAla--- 251
Db 7993 TGGAAGAGGCACCTGTAGTCACTGCTCAGCAATTTGGTCGATAGTTGGAATGATCTTTGC 7934
QY 252 ---Glu--- 252
Db 7933 TTTTATTTCCAGCAAGTCAATTTGTAAGGAACGACACGGAAGGTGTTGAGGAGAGTGAA 7874
QY 253 Phe---GlnTrp--- 255
Db 7873 TTCTGGAGTGAATAATCTCAATGGGATTTTACATCTCTTAAACATTTTGAAGTTTATCCA 7814
QY 256 ---Lys---TyrLys--- 257
Db 7813 AATTGATGGAATCCTCAATCTGTCAAGGGGACTATATAAGTCAGAGTCTGAAAGTTAGC 7754
QY 258 ---Asp--- 259
Db 7753 TTCTTGGAGAGCTGGAGACTGACCTCAATGCAGGCATGCTCCACAGAAATGTTGGAT 7694
QY 259 --- 259
Db 7693 TTCAGGAACAATGAATCCTTGTTCACACAGTGTTCACACTCTCAGCCACCTTTTGGGT 7634
QY 260 ---Lys--- 260
Db 7633 GGAATATTGCTCTGCAAGTCTGTATGTTTATAGCAGTCAGAGTCCACCAGTCAGAAAT 7574
QY 261 ---Arg--- 261
Db 7573 GTAGGTGACCACCTGTGTAAACTTGGCTTTACCAGAGACAAGCAGCGCTCCAGTTCGCC 7514
QY 262 ---LeuIle---Glu--- 264
Db 7513 CTGAATGTCCATTTGATAAATTCGGTCTCGTACATCTTCTAAAGCATCTTGGAAATGGGC 7454
QY 265 ---Gly--- 265
Db 7453 TTTTATTTGAGCCAAACCATCTCGCAGCAATCAACGACACACAGTACTTTGTGTCTTT 7394
QY 266 Lys---LysGlyVal---LysVal--- 271
Db 7393 GAGTTTTTCCAGGAGTTGGAGACCGTGGTTTTGAAGTCTTCTACCCACAGTTTTTAATGC 7334
QY 272 ---Glu--- 272
Db 7333 TTCAGTTTTCTGTGGAGTTCGAGAGCTTGGATTCAGCATTGATTCCTGAGTCATCTC 7274
QY 272 --- 272
Db 7273 ACGGATTTTGTGTTGTTTGTCTCAAACTGGTGATATCAAGGCTTTTCAACTTTT 7214
QY 273 ---Asn---Arg--- 274
Db 7213 CACGACATGTCAATCAATCTATTCTCAGTCTCTCAATGATATTTTGAAGACACTGCTTT 7154
QY 275 ---Pro--- 275
Db 7153 AATCCACTCGAGTGTCAATCAATAAACAACCAATTTATCATAGTAGTCTTTTATCTC 7094

QY 275 --- 275
Db 7093 AATTGCTGTAGCACATTAATTAGTTTCTGAAGAGGCTCACTCAGGCTGTATCTGTGGGC 7034
QY 276 ---PheLeu--- 277
Db 7033 CAACTCTATTGATTATCCATTAAACCTGGATTGTGGTCTACTTCTATATTTCTCAAT 6974
QY 278 ---Leu---IlePhe--- 282
Db 6973 TAACTCAGGACTATAACTCTAAAGATATGATTTTCTCAGTTACTTTAAAATCTTCAAT 6914
QY 283 ---Phe---Asn---ValSer---Glu--- 287
Db 6913 AAGATTCAATACAAAGATTTTGACACGCTCAATATGACACATTATTTCTTTGGAATAGAAAT 6854
QY 288 ---His---Asp--- 289
Db 6853 TGCAGTTCTCAGTTGATCTAAATGCAATGGGACATCAAGAGCTTCAATCTGTTGTTTAA 6794
QY 289 --- 289
Db 6793 CTCTGCAGCAAGCTGTTGAATGTCTATATATGAATCTGTGTTCTGAGATGCTGGAGTTT 6734
QY 290 ---Tyr---Gly--- 291
Db 6733 TTCTTGTATCTGGATTCTGATTGATATTTGGTATCCACATTTTGGATCCAAGACGCACC 6674
QY 292 ---Asn--- 292
Db 6673 ACTACTACTGATTTGGTTAAGTCAACATTTTCAACAAAATAATAGAGATTTATGGATTGA 6614
QY 293 ---TyrThr--- 294
Db 6613 TTTTGTAGATTTTACCGATATGACTGTTCTCGTCAAGCATTTTGTAGCTTTTCAATGAT 6554
QY 295 ---Cys---ValAlaSerAsn--- 299
Db 6553 TCTATCAATAATCTGAGCAATAGTCTCTTTTAAAGTCTGTGTCATCATAATTTATCTTAAT 6494
QY 300 ---LysLeu--- 301
Db 6493 ATACTGATCAAAATGTATCGGTATGTCTCAAGTTGAGAGAGTTTTCATTTCAAGTTGAT 6434
QY 302 ---Gly---His--- 303
Db 6433 TTTGGCACTATCTAAGGCAATTAGTACATCAITATCTGTAATTTCTATAGTTTTCATGAA 6374
QY 304 ---Thr--- 304
Db 6373 AGAAGTTAATTTTCTTGGCACCGACTTGTCTCTCCAGTCAGATGCATTCAGATA 6314
QY 305 ---Asn---Ala---SerIle---MetLeu--- 310
Db 6313 ATCATGAATCTGTGAGGAAGCTGTCTCAGGGCCACTCTATATTTCTCACAACACTGATC 6254
QY 311 ---PheGlyPro---Gly--- 314
Db 6253 AACACTGAGGCGTTGTAATTC---CCCTTCATGGCTTCCAGTAGACTTATTAATTCCTCT 6197
QY 315 ---Ala--- 315
Db 6196 TCGATTTCTCCAAATAATCTGGCAGGCTTTTGGAGAATGGGAGGCTGATAGTGTGGAC 6137
QY 316 ---Val---Ser--- 317
Db 6136 ATCTTGGTTCTTATCGTATTTTACCACAGCATCAATTTGTGAATTTCTCGGGCTCGTCAAA 6077
QY 317 --- 317
Db 6076 GGCATCATTTTATCTCCAGCTATTAAACAATTTGACAGGCTCTACTGTAGAAAACGGCAC 6017
QY 318 ---GluValSer---Asn--- 321


```
Db 6016 TTTAATCGAGAGTACAGCCAGAGGTGACGCCGTCACCTAAGCTCGATACCAATTTT 5957
|||||
QY 321 ----- 321
Db 5956 GTCTTTAGTGTGTAGGCTTCAAAATTCCTGGCTGTATATCTTTGTCAATTCAGGCTGGTCTT 5897
|||||
QY 322 -----GlyThr----- 323
Db 5896 GAAATTCAGCTGTGTCTGTTTCAGCTGGAGTCAGCAAGGACGACTGATGTGTGCTCAAG 5837
|||||
QY 324 -----Arg-----Ser----- 324
Db 5836 AGCTGACTGAGCTGTTCTTGTACAGGAGATGTGGCTCGTGGATCTTTGTAGTCATG 5777
|||||
QY 325 Arg----- 326
Db 5776 AGAGAAGGTAAAGTGCAGAGGTTCTGCTTCAACAGAAATTTACTGTATCTATCTGCCAGT 5717
|||||
QY 327 -----Cys-----Val-----TriLeu----- 332
Db 5656 AAACGGTGCAGCAACAAAGCGGAAACATTTGTTAAATGCGAGTGTGTCGACGCCCAAGGT 5597
|||||
QY 333 -----Leu-----ProLeuLeuVal----- 337
Db 5596 GGTAGTGATCATCAACGGAGGAAGCAGCCCTTCGATGTCTGCATTTAGCTATGCGCTGAA 5537
|||||
QY 338 LeuHis----- 339
Db 5536 CTCACACCTGAACCGTAGCTACAGTGTCTGCTCTGTAACCTGCTACTACCAGTCACT 5477
|||||
QY 340 -----Leu-----Leu-----Leu-----Leu-----Leu----- 343
Db 5476 ATAAGAGATGGTATAGATGTGTTTCAGCTCATTAATTTGGTAGTTCCTTTAAAGTTGCC 5417
|||||
QY 344 -----Phe 344
Db 5416 ACCCAATTCAGCTTCAGTGGTTTC 5393

RESULT 20
AY321317/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
XU,C.S., LI,W.Q., LI,Y.C., ZHAO,L.F., MA,H., WANG,L., WANG,S.F.,
HAN,H.P., WANG,G.P., CHAI,L.Q., YUAN,J.Y., YANG,K.J., YAN,H.M.,
CHANG,C.F., SHI,J.B., RAHMAN,S., WANG,Q.N. and ZHANG,J.B.
Liver regeneration after PH
Unpublished
1 (bases 1 to 14278)
XU,C.S., LI,W.Q., LI,Y.C., ZHAO,L.F., MA,H., WANG,L., WANG,S.F.,
HAN,H.P., WANG,G.P., CHAI,L.Q., YUAN,J.Y., YANG,K.J., YAN,H.M.,
CHANG,C.F., SHI,J.B., RAHMAN,S., WANG,Q.N. and ZHANG,J.B.
Direct Submission
Submitted (11-JUN-2003) Henan Bioengineering Key Lab, Henan Normal
University, NO. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.
China
FEATURES
Location/Qualifiers
1..14278
/molecule="Rattus norvegicus"
/mol_type="mRNA"
```

```
/db xref="taxon:10116"
41..14272
/note="liver regeneration related protein LRRG183"
/codeon start=1
/product="Acl-060"
/protein_id="AAP86249.1"
/db xref="GI:32527695"
/translation="MGFORALRAPLILLLFLDPSVMAQDAPRPHLRKLVYVSE
AESGVRGADRSATKINCQKVELEVPQVCTLLIMRTSQCTLKEVYGFNEGKALMK
TKNSPEASAMSRYELKAPFEGKVALYIPDLGEPNLYILKRIISALLVPPTEED
KQVLFQDTVYVNGSTQVTVNSRGTATENSTERNLQHCDFQFISTSVSLALIKGL
VRLSTLISSQSCQVTLPEKPKHSEAIQNEOHLFLFFYKKNKYGMTVTKLSLE
DKPNSRFFRGGINQGLAFESTKSPPKQADAVLKTQLQELKGLSISQNAORANL
FKLVTLRGLSGEATISLLPOLIEVSSPITLQALQCGQPECVTHILOMLKTEKAP
LLIDIVYIMALLPNSVQRLQELFNTAKELQSRATILYALSHAVNSYVLMDSRSPV
LEDIAYLMQIDNECGDEBRTFLIRVIGNMGRMTWRVMPALCKSSVYALCKSRFS
LQKQALQALRKMEDGVRTILFDTFVNDVAPVEKRLAAYLLLMSPSSPSSDINKIA
KLQMEQSEGVNFVASHIANIINSELYVQDLKNLIKALVNSRLPTIMDFKFSN
YQISKVSIPLFDPVSAKIBGNLVDPSSVLPKESMLKTLTVFGIATSLDFEIGLSE
GIMPIVDKLIKELKEIPERAYILRLGELGFVRLQDLQVILKLLINGAQTPRGVP
KGPEPTLEALFGKGFPPDSVNKALYVWNGOVPRYSKVLVDHFGYTKDQKHEODWYN
QMVQALREGSKODLFILHYIPMENAFELPTGVGLQVQSSGVNTFFHESGLEARVALKAGQULVIL
IOAELVAKPSVLEFVTNMGIIIPDFAKGVQMNNTFFHESGLEARVALKAGQULVIL
PSRKPVKLFGSNTLHLVSTTTEVIPLEIENRKSWCTCKPFTGNYCTYGAQSV
SSTESASYPLTGDTRYELKPTGEVQYASATYELKEDSLVTLKFLVQAEQV
QGEATAMFKYNNRSRTLSSEVLIIPGPDVNFGTILRVNDESSKDKNTYKILDIQNK
ITTSVGVHVSVDKGGKGVGVSIIPRQAEARSEVHTHSPTKLLFOWDSSATAGV
ITTSKVAWRIDNEKIEFDWNTGVNTDKKVASFPVDSLRYSYPAWHEAYANGLLDHRV
PQDMDPRHMGSKLIVDLHNGLSNELNPKVGLPDPFHIDNLFTDRGRVYKTLNKNRI
EIDIPPLGKSKDLKAPESVTRPALNPKSVGFHLPSQEVQIPTFTPKTHQVPL
LGLIDSTNYVSNLYNMSVGTGSRDHFSLQAQYVMKADSVVDLFSYVQSGSAT
TYDSKFTLSCDGLSHHFLDKSKFVSHVEKFNPNVSKGLLTFTSSALGPOMSAT
VOLDKKOHLVYKDIKVDQFQVPSLYAQEYGLSVERDSMTQSGMSQENKFNSTY
FQGTQVQVMQDGLSTSDLOGIIPNTASLKYENYELILKSDSSQENYENPAAS
NKDMDTSKALLRSHQANYKLRLLTLLSGLSYQVLELNLADLIGTDKINTGAKH
STKALTEVSGYSTATTNLKSPILLENELNAELSGAKMLSGTSFGEKHAHAKFSLR
IGSLDNFPGSKMDNIYSGDKPYQNFLOQYSPGITLSDVTVASVRADTVATVQGVFHRNLADLE
EPKILNVGNGKGTQYNNELKILYTSITDVLVAVSRADTVATVQGVFHRNLADLE
GLASSVDVTSYSSDPLHFNVPFVLAPITLGVDTHTSGDGLSGEHTGQMSKE
LLKAEPLALTFSDKIGTSHNLILKNSVSTALEHTLSALLTPPAVNSWKFKTSLMD
KVSQEFENATDKDIGELSGRADSLGSPYKVPFFYSEPVNVLNSLEINDAFDEP
REFTIDAVKYDKNQDVTISLPFPQSLPDLERNRGGIISLEAMEGLQRLSDVDF
VRKYVALSRPLQOIHDXLNASOWERQVAGAKELTSMENYRITMDNLVIALDSAKI
NLNEKLSOLETYAQFOQYTRDNYDAQDLKRTIAQIDRLIEKLMDQEOVTHIRVNIA
KSILNLYLFVENDLNOISSGASWIONVDTKQIRIQIOELKQHLRTOIHNIDQIL
AELKQOIALDVPMDLQRLTALFORISVIERVKYFVNNLIEDFKYTEKINTFRV
IVRELIEKYEVDROIQVMDKRSIELAHRSLSLEPLQKLSNVLQIIRIKOYDKLVGFI
DDTVEWIKAVSFKNIBELANRLDMSVKKLKAFDYHQFVDTKNSKIREMTORINAEIQ
ALDELQKTEALKLWVEDKTVSNLSLEKADKTVVTVVWLDQDLAQIKAQFQDALIED
VRDRIYQMDIQGELERCLSLVSOYVTVTVISDWMTLTAKNIIDFAOYSTQKWAES
VKALVQGFIVPEIQTLGTMPAPEVSIHALQEAENFOTPDFIVPLDRLRISWINFK
MLKNVGLPREFSTPEFTLNTFRVRSSTIDILEIKAKIRITDMLSELOPLPEVY
LRDWMENIISLARUSLDFHVFETIPEFTIPNVNLDQVDDHIEFQFQPLSCCTT
IIPAFGLHSLVLIQSPFLFDASANIQTTSSENKAEIVASVYARGESPEALNDFD
QAQAFLELANPLVSKESVNFSSKHYRMEHEGLVSGKALEGSTVPLARLTKNT
VTFNNNGACPNFSDGTHSSKISPIVDGPIASGLSNNINGKRVVQKLTTSRSGFLN
GTGNNWACPNFSDGTHSSKISPIVDGPIASGLSNNINGKRVVQKLTTSRSGFLN
YSREVSQSVESQVGSILTAEGRALLGDAKAMTGEHNNANLKVIGTLKNSLFS
AQPFETASTNNEGNLKVSPDKIKDILFNLYALFUSHAQASQWLSQSTFRFQYKI
NONFSALNNEHMEASIVMNGDANLDFNLPTIPEINLPTFRFTLTKDQFSTWET
GLKFLTKTKQSPDLSIKAYQKGRDKSVVILPKMFYEFMLNNSWDRKFEKVRDN
ALHETASYNETKIKDKYKNTENSINQPSRTFQNRGHTIPVNLIEVSPFAVETLASH
VIPKAITPSTVITPGPNIIVPSYRLVPSLQLPVFIPTLFLKSLQDFPKKLTSTLRI
YIPAMGHTYDPSFKSVIPLTNTAGLYNQSDIVARFLSSSFYTDALQKLGSTGDI
MRKVKLATASVLTNFKLKGSHDSTISLTKNMEASVYKTLANLHAFITPNFQELN
FLTSKPTVSSSIEINLVDFNSKLSAAKGVGDHFKFSLESLSYLSFSTFKNGIKGS
GNTQSGSVANEANYINSGTSSSVLRQASNFAGIWNFEVGENFAGEATERRIY
TWEHMLNHLQVFSYFDTKQTCRATLELSPTMTSTLLOHVHVSQSPFLFDLHFDQ
VILKASTKQKVSQVSVESOVLOHNAHESNDQEEVRLDIAGSLQGLWDLNFFFL
PARGKSLRELQIDQKQYLOASTSLHYTKNPNGLYLLSPVQELTDFELIPLGLNDF
SGIKLYKSLSPFALNLTMLPKVYFQVLDLLTOYSKPESSSVTFTTPIBQILTWS
QFTLPKSPFVGNVTVDLNLKNTLADVDLPSTLPEQTIETIPLSEFSPVAGIIPFFFG
```

ELTAHVGMASPLXNVTVTGWKKNKADHVTETLDSTCSSTIQFLEYALKVVGTHRIEND
 KFIYKIKGTILQHCDFNVKYNEDGIFEGILWLEGEAHLIDITSPALTEPHLYKEDKTSV
 SASAASPAITGVSLDSDQSVLNVYFRPQSPDNKLSIFKMEWRKESDGETYIK
 INNEEAAFLRLSLKSNVPSKASEAVDYVKKYHLGHASSELKSLQNDABHAIRVMD
 EMVNAQRVTRDTYSLYKXLAQESQSIPEKLKMWIGSLVRITQRYHNAVTLWMD
 VILHFNQRVQFPNGACTYVDELYTTAMRETKKLSQLFNGLGHLPFSYVQDOVKSR
 VINDITFKPSPPTCKLDVLLIFREDLNLNLGQODINFTTILSDFOSEFTELRLD
 IIEEKIFLKNNESTCVPDHINMFKTHIPAFKSLRENIYSVPSENFDFQSTLQBG
 SYKLQVQYQMKAFREYFPDPSVVGTVTKYIEEEKWDLIKLILAPLRFYSEYVT
 AADFASQSTOVQFVSORDIREYLSMLADINGREKVAELSIVVERIKSWSTAVAB
 ITSDYLRQLSHKLSQDFSDLSGYEYKFEASTRLIDLSIQNYHMFLEYIAELKLCQV
 ATANGLLKRGDPEAAVKGLIACLYNEGLSVDEAYAVNGLXASRFFSMDERLWMS
 DPFILWISICPCPKRDFAGKWEAQPALADKAGCSQGLGEGRAFSESVQOLFQA
 SOAVNQKQIFSVOKGLSDTVRYLILGLWVEVAPMKOFTSLCLHLTVECVGRYLQKLV
 PRYKLOLLGIACWICWTFWISKELLITREAVRLTDNYKYKDIVRVKREILISALEGKI
 RIFTVVDYKEVLLVFPVTPERTQYLCFLCELTLVSVPYPAHLASAALLLRLMHGQTQ
 P"

ORIGIN

Alignment Scores:
 Pred. No.: 3, 81e-12 Length: 14278
 Score: 1679.30 Matches: 283
 Percent Similarity: 11.44% Conservative: 45
 Best Local Similarity: 9.87% Mismatches: 13
 Query Match: 69.74% Indels: 2527
 DB: 11 Gaps: 239

US-10-017-084a-523 (1-344) x AY321317 (1-14278)

QY	1	Met	-----Lys-----Thr-----	-----	3
DB	13987	CTCTTTGCTGATGAACCAAGGTACAGATGACCATCAGGCAATGCCAGAGAGCTGGAGCTT	13928		
QY	4	Ile	-----Gln-----Pro-----	-----Lys 7	
DB	13927	GTATCTGGGACCAGTTTCTCTCAAGTAGCCGGCCTACACTCCACTGTCAGGTGAAG	13868		
QY	8	-----MetHis-----	-----Asn--- 10		
DB	13867	ACACAGCTTGTGAGTCTTTCATCTGGGGCACTTCCACCAACAGCGGATTAGATGTA	13808		
QY	10	-----	----- 10		
DB	13807	CCTCAGGTGTCACTGAGCCCTTCTGCACAGAGATATCTGCTGTTGTGACGGCTG	13748		
QY	10	-----	----- 10		
DB	13747	GGAGGCTTGAAGAGCTGACAGACCGACTCACTGAAGGCCTTCCCTTCTAGTCCAAGCTG	13688		
QY	11	---Ser---	-----Ile-----	-----Ser 13	
DB	13687	GCTTCCACCTGCACAGCTTTTGGCCAAAGCGGCTGTGCTTCCACAGCAGCTTTGCCAGC	13628		
QY	14	-----	-----Tyr-----	----- 14	
DB	13627	GAACTCCCTGAGTTTCCGGAAGCATGTGTGGGCAGATGGAGAGCCAGATGAAGGGTCTGA	13568		
QY	15	-----	-----AlaIle---Phe 17		
DB	13567	ACCATATTCAATCTCTCGTCCATGCTGAAGAGCGAGAGGCGCTTCAGGCGCATTCACCTC	13508		
QY	18	---ThrGlyLeu---	-----Ala-----Leu 23		
DB	13507	CGCTAGGCTCTGTCGACACAGACAGAGCTTTCATTTGTAGAGGCGAGGCGATCCCAACTT	13448		
QY	24	-----	-----Cys----- 24		
DB	13447	CACAGAGCTTCAAAATCCCCCTTTTTCAGCAGGCCATTATTGGCTGTGGCCACCTGCAG	13388		
QY	25	LeuPheGln-----	----- 27		
DB	13387	CTTTTTCAGTAACCTCAGGATGTATCTGAGAAACATGTGGTAGTTTGAATGGACAGGTC	13328		

QY	28	-----Gly-----	-----Val-----	----- 29	
DB	13327	AATCAGCTTGTGGACTCAGCAACGAATTTTTCATAGTACCCAGAGAGCTGGTCTGAAA	13268		
QY	30	-----	-----Pro---Val-----	-----ArgSer 33	
DB	13267	ATCCTGCAGTTTGAATGGAGCTGCCGGAGGTAATCAGACGTTATTTCTGCCACCGCAGT	13208		
QY	34	GlyAspAla-----	-----ThrPhe-----	-----Pro 39	
DB	13207	GGACCGACTTTTATTTCTTTCCCTTTTACCAACAATAGAAAGCTCTGCAACCTTTTCCCTCCC	13148		
QY	40	-----	-----Lys---AlaMet-----	-----Asp----- 43	
DB	13147	CTTTCCATTTATGTCAGCAGCATGCTAAGATACTCTCTGATATCTCCTGGACACAAATTTG	13088		
QY	44	---Asn---	-----Val-----	-----ThrVal----- 47	
DB	13087	CTCAACCTGAGTTGACATTTTGGGAAGCAAAATCAGCAGCTGTCCACTGTATTTCAGAGTA	13028		
QY	48	-----	-----Arg---Gln---Gly---GluSerAlaThr---Leu-----	----- 55	
DB	13027	GAAATCCCTCAGAGGAGCCAAAAGGCTCTTGATAAGGTCAACCATCTTTTCTTCTATTTC	12968		
QY	56	-----ArgCys-----	-----Thr-----	----- 58	
DB	12967	ATAATATTTTACTGTCCAGCAACACACTCGGATCAAAATACTCTTTCAGAAAGGCCTT	12908		
QY	59	---Ile---	-----Asp-----	-----AsnArg 62	
DB	12907	CATATCTGATGACCTGCTGCTAGCTTATAGGACCCCTCTTGAAGTATGGATTGAACAA	12848		
QY	63	Val-----	-----Thr---ArgVal-----	-----AlaTyr 68	
DB	12847	GTCAITTGAATCTCACTGAAGCAGATATATGTTTCTCTCAGGGATTAAATGCAATGG	12788		
QY	69	-----	-----Leu 69		
DB	12787	GATATGTGTTTGAAGAACATGTTGATATGATCAGGACACAAAGTAGATTCAATGTTCTT	12728		
QY	70	-----Asn---	-----ArgSer-----	----- 72	
DB	12727	TAGGCATTCAAATTTTCTTCTATGATGCTCAAAGTCTCTCCAAAAAGCTCTGAAAGTC	12668		
QY	73	Thr-----	-----IleLeuTyrAla-----	-----Gly----- 78	
DB	12667	ACTTAGTATTGTTGTAATAATGATATCTCTGTGGCCTAAAGTTGGATAAAATGTTTAAGTC	12608		
QY	79	-----Asn---	-----Lys---Tyr-----	----- 82	
DB	12607	CTCCCTGAAAATCAATAGGACATCTTTTAGTTTACAGGTTGTTGGGAAAAGGACATTT	12548		
QY	83	---CysLeu---	-----Asp-----	----- 85	
DB	12547	AAATGTTATGTCTATTGATTACTCTTGATTTTCTCTACTGTCTTGAACATAGGAAAACAG	12488		
QY	86	-----Pro---	-----Arg-----	----- 87	
DB	12487	GTGTCCTAACCCANTAAACAGCTGAGAGAGTAACCTTCTTGGTTTCCCTCATGGCTATAGT	12428		
QY	87	-----	----- 87		
DB	12427	GTAAAGTTCTGCCACAGTATATGTTCCAGCATTTCCCTGGAACTGGACTCTATTGAACTT	12368		
QY	88	-----	-----ValValLeuLeuSerAsn 93		
DB	12367	CAGGAAATGAATGACTGAGTCCATCAGCATGTGACTGCCATCTGTGCTACTTCTGAGTAAT	12308		
QY	94	Thr-----	-----Gln---Thr-----	----- 96	
DB	12307	ACGTACTAGATGCGCTAAACACCATTTTCTTGTAGTTTCTCAGGGATACTCTGGCTCTCCTG	12248		
QY	97	---Gln---	----- 97		

```

12247 AGCCAAACATCTTCTATATAGACTCTGGTAGGTATCACGGGTACCCCTCTGGGCATTAC 12188
      |||
QY 98 -----Tyr-----SerileGluLe----- 102
      |||
12187 GTTCATCTCATCAACCATCTTATGGTGTTCAGCATC---ATTCTGAAGACTTTTTCT 12131
      |||
QY 103 -----Gln-----Asn----- 104
      |||
12130 TAGCTCTGAAGAAGCATGCCAGGAGGTACTTCTTGACATANTCATAAACAGCCTCAGA 12071
      |||
QY 104 ----- 104
12070 AGCCTTGGGCACATCTCTTTTAGGGAGTCTAGCAATCTGAAGCTCTTCTTCTCCCA 12011
QY 105 val-----AspVal-----Tyr 108
      |||
12010 GTTAAATTTGATGATATGTTTTCACCATCAGACTCTTGTCTCCCTCCATCCCATTTTGAATAT 11951
      |||
QY 109 -----Asp----- 109
11950 GCTGAGTTTATATCTGGAGGGAGCTGAGGGCGGAAGTAGACATTCAGCCTCACACTCTG 11891
      |||
QY 109 ----- 109
11890 GTCATCTGTCTTGCATCCAGACTCAGATGCTTATGGTGGGGAGGCTGCTGAGGCAGA 11831
QY 110 -----Glu-----Gly--- 111
11830 CACACTGTCTGTCTTCTTTGTAGTGCAGATGGAAGTCAATCAGTCAAGTCTGGGTGTGAT 11771
      |||
QY 112 -----Pro-----TyrThr----- 114
      |||
11770 GTCCAGATGAGCTCTCCCTCCCAAGTCCCAAGTCTTCAAAATATACCATCTTCGTTATA 11711
      |||
QY 115 -----CysSer----- 116
11710 CTTACATTGAAGTCACAGTGTGAAGTGTCTCTTTGATTTTATAGATGAATATATCAT 11651
      |||
QY 116 ----- 116
11650 TTCAATCCTGTGTCTCCCAACTTTTAGAGCATACTCCAGAACTGCAAGTTGAAC 11591
QY 117 -----ValGln-----Thr----- 119
      |||
11590 GCATGTGGAATCCAGGAATGTTTCAACATGCTCTGCTTGTGTTTTCACACCACTGCTCCA 11531
      |||
QY 120 -----Asp-----AsnHisPro----- 123
      |||
11530 CGTGACATTATACAGGGGAGAGGCCATCCCAACGTGTGCAGTCAAGTCTCTCCAAAGAACGG 11471
      |||
QY 124 -----Lys----- 124
11470 AATAAAAAATCCAGCAGGTACAGAGAAGTCAAGGATGGATCTCAATGCTGTGCTCG 11411
      |||
QY 125 -----Thr----- 125
11410 CAGGGTGATAGTGGCAGATCAACATCTGCAATTAGGTGTTGTTAGCTTATTCAGATCAAA 11351
      |||
QY 125 ----- 125
11350 GACAGTGTTCGCAACGGGAAGCTCTTTGGAAGTGTAACTGGGACACAGATTAAATTGAAT 11291
QY 126 -----Ser-----ArgVal----- 128
      |||
11290 TTCAGGTATAGTTGTTCTCAAAGGTAGGACAGAGAGGCCCTCTGTTTAGAGTATTGTTG 11231
      |||
QY 129 -----His----- 129
11230 TAAACAGATCAACCCCGAGGAATTTTACTTTGGGAGCATTGTTAGTTGAGGGCAAAATGG 11171
      |||
QY 130 -----Leuile-----Val--- 132
      |||
11170 TGAAGTACTTAATTTCTTATAGATTTTGTATCCACTGAAGTCATTTAGTTTCAGCCCTGG 11111
      |||
QY 133 -----Gln----- 133
11110 TATAATGAATCTATCAGTCAGTTCTTTCACAGGAGTGAAGAGATAGCCATTCCGGTT 11051
      |||
QY 134 -----Val-----Ser----- 135
      |||
11050 TTTGGTATAGTGAAGAGAAGTGAAGCTTGAAGATACTGACGCTTCCGCTCTATCTGTAG 10991
      |||
QY 136 -----Pro----- 136
10990 GAGTTCCCTCAAGCTCTTGCCAAATGCCGTAGAAAGAAATTTTCAAGTCCACAGCTG 10931
      |||
QY 137 -----Lys----- 137
10930 TCCTTCTAAGGATCCAGCAATGTCAAGCGGTACTTCTTCTTGGTCATTGGAGAAGTGTGC 10871
      |||
QY 138 IleVal----- 139
10870 ATTGTCTGAAGAACCTGTGATTCAACCTGGACCTCATTTCACAGCTGACCTTCTGTT 10811
      |||
QY 140 -----Gluile----- 141
10810 CTTAGTGTAGCTTTTCAGGATCATTCTCTGTCAAAGTGAATGAGATCAAGAGGGGACT 10751
      |||
QY 141 ----- 141
10750 GGGTGACTCACATGAACCTGTAGAAGGGTTCACATGGTCCATGGGAGAGCTTAGGGT 10691
      |||
QY 141 ----- 141
10690 GGCCTCTGCATGTTTGTCTTCTTGTCTCAAAGTGAATACCTGTAAATGTTTAT 10631
      |||
QY 142 -----SerSer----- 143
10630 CATATTGTGTTCCCATGTGCCATAGATGCTGGAGAGTAGCTTCTCCAGCAAAATTTTC 10571
      |||
QY 143 ----- 143
10570 TCCTACTCAAAGTTCAGATCCCAAGAAAATTAGAGGCTCCTTGTAACTTACTGAAGA 10511
      |||
QY 143 ----- 143
10510 CCGAGTACCCTTAGAATTCAGGTACACATTCGCTCATTTGGGACACATTCCTGAATATTC 10451
      |||
QY 144 -----AspileSer----- 146
10450 CTGTGAAAGGAACGAACCCCTTGATATTTCTTTGGTGAATGACTCAATGGAAGGTAGGA 10391
      |||
QY 147 -----IleAsn----- 148
10390 AGTGAGACTTCTTAAGCTGAACCTTGTGATCAACACCTCCTTTTGTGTCAGAGTGCAGCTT 10331
      |||
QY 149 -----Glu-----Gly 150
10330 TGAGGAATTTGAAGTCATAGTTTGTGTTCAATGGAGGATGAGACAGTGGGCTTTGACTGTT 10271
      |||
QY 151 -----Asn----- 151
10270 GTTTCGGTTAAGTTCCTGTTGAAGTTTCAATGTGTAATATGGAGCGTGGAGTTGGCAGT 10211
      |||
QY 152 -----Asn----- 152
10210 TGTTTTCTAGTGAAGCTTCCATGTTTTTCTTGTTAAGCTAAATGGTGTCTCATGACTTCC 10151
      |||
QY 153 -----IleSer-----Leu----- 155
10150 CTTTAAAAATTTGTTAGTTAGAGACAGCGGTGGCTAACTTCAATACTTTTTTCCGCAT 10091
      |||
QY 156 -----Thr---Cys-----Ile----- 158
10090 CAGACGTGATGTACCTCTAGTTTGTACTGACGGGCATCCGTGACAAATGAAGAGGAAGA 10031
      |||
```

QY 159 ---AlaThr---Gly--- 161
Db 10030 AAGAAACGACGACGAGATCTGATGGTTATAAGTCCAGCATTTGGTATTCAGTGTGAT 9971
QY 162 ---Arg--- 162
Db 9970 GACACTTGATTTAAAGAAAAGTCATAGGTGAATTTGCCCATGGCTGGGTGAATATAATATT 9911
QY 163 ---Pro--- 163
Db 9910 GTCAATAGTCTTAATTTCTTGAATCTGGAGGGAAAACTTGAATAGAGTCCCTAGGGAT 9851
QY 164 ---Glu---ProThr---Val 167
Db 9850 ATGGAAGCTGGCAACTGTAGACGCGACACTTAACCTGTATGAGGACAAATGATGTT 9791
QY 168 ---Thr--- 168
Db 9790 AGGACCTGGAATTTGACGCTTGGGTGCGGATTTCTTCGGGATCACATGGCTGGAAGC 9731
QY 169 ---TrpArgHis---IleSer--- 173
Db 9730 CAGTGTCTACAGCAATGGACACCTTCAATGTTGAGAACTGGGATGATGTGTCACG 9671
QY 174 ---Pro---LysAlaVal---Gly---Phe--- 179
Db 9670 AATTTGAAAGTCTCGAAGGCTGATTGAGGGAATTTTCAGTTTGTACTTATCAAACTT 9611
QY 180 ---ValSer--- 181
Db 9610 AATTTGTTTCAATPAGATCGGTAAGAAATGTAATGTCATGTCCTGACTTTCTC 9551
QY 182 Glu---Asp---Glu--- 184
Db 9550 AATTTTCTCTCCAGAAATGACATTTGTTGAGCATAACTCATAAACATTTTCAGAGG 9491
QY 185 ---Tyr--- 185
Db 9490 GATAACAACAGATGCTGTCTGTCTTTTATATTGAGCCTTTATACTCAAGTCMAA 9431
QY 186 ---Leu--- 186
Db 9430 TGACTGTTGTTGCTCTCAAAAATCTTTCAAGCCGTTTCTTCCCATATGGAGAAATC 9371
QY 189 ---Gln---Gly---IleThr---Arg 193
Db 9370 CTTCAAGTAAGGAGTTGTGAACCTTGTGTAAAGGTAGATTAATTTTCAGGAATTTGTTAAGG 9311
QY 194 ---Glu---Gln---Ser---Gly--- 197
Db 9310 TATGTTTAAGAAATCAAGGTTGGCATCTCCATTTACTATCTACTGCTTCCATGTTGTG 9251
QY 198 ---AspTyr--- 200
Db 9250 CTCAATGTTTATAGCGGAAAAATTTTGATTTGATTTGTAATTTGTAATGTAATCTAGTACTCAA 9191
QY 201 ---Cys--- 201
Db 9190 TTGCAGCTTGTCTTGTGGCATGGGGCTCAGAAACAGTGCATAGTATTTAGGAAGTC 9131
QY 202 ---SerAla---SerAspValAlaAlaPro---ValVal--- 212
Db 9130 TATTTTCCAGTCAACTTTTAGTGGAAAACTAAC---TTTCAAAATTCCTTCAATATTGT 9074
QY 213 ---Arg---ArgVal---Lys--- 216
Db 9073 GGATGCGATTAATCTCAAAATGGTTGTGCCGAAAAAGAAAGAAATTTTTCACGTTCCAAT 9014
QY 217 ---Val--- 217
Db 9013 AACTTTTCCATTTAAGTTGGCATTTGTCTCACCAGTCAATTTCTGCTTTTGATCCCCAAG 8954

QY 218 ---Thr---Val--- 219
Db 8953 CAGTGGCCGACCTCTGGCAGTTAGAAATGCTGGAGCCACGCTGAGATTCAACTTTTGA 8894
QY 220 ---AsnTyr---Pro--- 222
Db 8893 CTCAACTTCAACCTAGAAATAGTTGAGGAAGCCAGATTCAGAAGTCAGTTTGGGACAAC 8834
QY 223 Pro---Tyr---Ile---Ser--- 226
Db 8833 CCTTAGTGTGTTGCCATTTATGTTATTGGAACAATCCAAAAGAACCAATGGGGCCATCCAC 8774
QY 227 ---GluAla---Lys---GlyThrGly---Val 233
Db 8773 AATGAAGCTAAATTTTGGATGATGCTTCACTGAGAAGTTGGGACAGGCCAGTT 8714
QY 234 Pro--- 234
Db 8713 CCATGACCTGTCTGAAAGATCCATGCCATATGTCAGCTTCTAATAGTGTCTTTGAT 8654
QY 235 ---Val---Gly---Gln--- 237
Db 8653 TTCATTGTTGAGAGAACCTTACTGGAGAAGTCCAGCTTGGGACACTCAACTTGTGGAA 8594
QY 237 --- 237
Db 8593 GTACTTTGTTGACTGTCAAGGTGAATTTGTTTATCTTGCACAACTAATACCATATT 8534
QY 238 ---Lys 238
Db 8533 AAATCCACTGATTTTCTCTGTGTAACTTTGCAACGCTGTCTGATTTTCCCTCAAG 8474
QY 239 Gly---Thr--- 240
Db 8473 GGCTTTCCAGAACTAATATCTTACCCTCATGCTCCATCTTCACATGTTTACTGGAGAA 8414
QY 241 ---LeuGln--- 242
Db 8413 GTTCAAGGATTCCTTCAGTACCAGAGGATTAGCATTTAACTCCAGGAACCTGAGCTGTGC 8354
QY 242 --- 242
Db 8353 TTGAAATCAAAATTTGAGAGCTTCAAAATTTGGACTCTCTCTGGCAGTGCACAGAAGCCAC 8294
QY 243 ---Cys--- 243
Db 8293 AATCTCTGTTTCTCTGAAAGTAGTATGTTCTGTATGTTGGCACTAGCATTAATAT 8234
QY 244 ---Glu---Ala---Ser 246
Db 8233 AAAGGGGAGATTGGATTTTCAGGAGCTATGATGTTTGGCGAAAGCAGGTATTTTCAGT 8174
QY 247 ---Ala--- 247
Db 8173 TGTGCATGAGGTGAGGAAGCTGGAATTTCTGTATGTGAAGATCAGGAACCTGTAATATC 8114
QY 247 --- 247
Db 8113 TTTGAGATTGACATTTGGGATTTGTGAATTTCTGGAAATTTGATTTCTGTGTACATGGAAGTC 8054
QY 248 ---Val--- 248
Db 8053 TGSCAGAGAGAGTCTTGCAAGAGAAATGTTCCACCATCTCCAGGTCTCTCTCAAATACACTTC 7994
QY 249 ---Pro---SerAla--- 251
Db 7993 TGGAGAGGCCACTGTAGCTCACTGCTCAGCATTTGGTCGATAGTTTCGAATGATCTTTGC 7934
QY 252 ---Glu 252
Db 7933 TTTTATTTCCAGCAAGTCAATTTGTAAGGAACGGACACGGAAGGTTTGGAGGAGTGA 7874
QY 253 Phe---GlnTrp--- 255

Db 7873 TTCTGGAGTGGAAATCTCAATGGGATTTTACATCTTTTAACATTTTGAAGTTTATCCA 7814
||| |||||
QY 256 -----Tyr-Lys----- 257
||| |||||
Db 7813 AATTGATGAATCCTCAAAATCTGTCAAGGGACTATAAAGTCAGGAGTCTGAAGAGTAGC 7754
||| |||||
QY 258 -----Asp----- 259
||| |||||
Db 7753 TTCTGGAGAGCGTGAGAGTCTGACCTCAAAATGCAAGCATGGTCCCCAGAAATGTTTGGAT 7694
||| |||||
QY 259 ----- 259
Db 7693 TTCAGGAACAATGATCTTGTTCACACAGTGTTCACACTCTCAGCCACTTTTGGGT 7634
||| |||||
QY 260 -----Lys----- 260
||| |||||
Db 7633 GGAATATTGCTGCAAAAGTCTGTATGTTTTTATGAGTCCAGAGTCCACCAGTCAGAAAT 7574
||| |||||
QY 261 -----Arg----- 261
||| |||||
Db 7573 GTAGGTGACCATGCTGTAAACTTGGCTTACCAGAGACAAGACGCGTCCAGTTCCCC 7514
||| |||||
QY 262 -----LeuLeu-----Glu----- 264
||| |||||
Db 7513 CTGAATGTCATTTGATAAAATTCGGTCTCGTACATCTCTAAAGCATCTTGGAAATGGGC 7454
||| |||||
QY 265 -----Gly----- 265
||| |||||
Db 7453 TTTTATTGAGCAAAACCATCTGCAGCAATCAACGACAACAGTCTTCTGAGTCTCTT 7394
||| |||||
QY 266 Lys-----LysGlyVal-----LysVal----- 271
||| |||||
Db 7393 GAGTTTCCAGGAGTTGGAGACCGTGGTTTGAAGTCTTCTACCCACAGTTTAATGC 7334
||| |||||
QY 272 -----Glu----- 272
||| |||||
Db 7333 TTTCAGTTTCTGTGGAGTTCGAGAGCTTGGATTCAGCATGATCTCTGAGTCATCTC 7274
||| |||||
QY 272 ----- 272
Db 7273 ACGGATTTTGTGTTTGTCTAACAACCTGGTGATTAATCAAGGCTTTCAACTTTT 7214
||| |||||
QY 273 -----Asn-----Arg----- 274
||| |||||
Db 7213 CACCGACATGCAATCAATCTATTCAGTCTTCTCAATGATATTTTGAAGACACTGCTT 7154
||| |||||
QY 275 -----Pro----- 275
||| |||||
Db 7153 AATCCACTCGACAGTGTCTATCAATAAACCACCAATTTATCATAGTAGTCTTTTATCTC 7094
||| |||||
QY 275 ----- 275
Db 7093 AATTGCTGTAGACATTACTAGTTTCTGAAGAGGCTCACTCAGGCTGTATCTGTGGGC 7034
||| |||||
QY 276 -----PheLeu----- 277
||| |||||
Db 7033 CAACTCTATTGATTATTCATTAACCTGGATTTGTGGTCTTCTATTTCTCAAT 6974
||| |||||
QY 278 -----SerLys-----Leu-----IlePhe----- 282
||| |||||
Db 6973 TAACTCAGGACTATAACTCTAAAGATTTGATTTTCTCAGTTACTTTTAAATCTTCAAT 6914
||| |||||
QY 283 -----Phe-----Asn-----ValSer-----Glu----- 287
||| |||||
Db 6913 AAGATTCAACAAAGTATTGACACGCTCAATTAATGACACTTATTTCTTTGGATAGAAT 6854
||| |||||
QY 288 -----His-----Asp----- 289
||| |||||
Db 6853 TGCAGTTCTCAGTTGATTAATGCAATGGGACATCAAGAGCTTCAATCTGTGTTTAA 6794
||| |||||
QY 289 ----- 289

Db 6793 CTCGCGCAAGCTGTTGAATGTCTATATTATGATCTGTGTCTGAGATGCTGGAGTTT 6734
||| |||||
QY 290 -----Tyr-----Gly----- 291
||| |||||
Db 6733 TTCTGTATCTGGATTTCTGATTTGATATTGTTATCCACATTTTGGATCCAGACGCCACC 6674
||| |||||
QY 292 -----Asn----- 292
||| |||||
Db 6673 ACTACTACTGATTTGTTAAGATCAACATTTTCAACAATAAATAGAGATTATGGATTGA 6614
||| |||||
QY 293 -----TyrThr----- 294
||| |||||
Db 6613 TTTTGTAGATTTTACACGGATATGATCTGTTGTCGTCAGCATTTTGTAGCTTTTCAATGAT 6554
||| |||||
QY 295 -----Cys-----ValAlaSerAsn 299
||| |||||
Db 6553 TCTATCAATAATCTGAGCAATAGTTCTTTTAAAGTCTCTGTCATCAATAATTTCTCTAAT 6494
||| |||||
QY 300 -----LysLeu----- 301
||| |||||
Db 6493 ATACTGATCAAAATGTATCGCGTATGTCCTCAAGTTGAGAGAGTTTTCATTCAGTTGAT 6434
||| |||||
QY 302 -----Gly-----His----- 303
||| |||||
Db 6433 TTTGGCACTATCTAAGGCAATTAGTACATCATTTATCTGTAATCTATAGTTTTCATGAA 6374
||| |||||
QY 304 -----Thr----- 304
||| |||||
Db 6373 AGAAGTTAATTTTCTTGGCACCAGTACTGTTCTCTCCAGTCAGATGCAATTCAGATA 6314
||| |||||
QY 305 -----Asn-----Ala-----SerIle-----MetLeu----- 310
||| |||||
Db 6313 ATCATGATCTCTGAGGAAGCTGCTCAGGGCCACTATATATTTCTCACAACATGATC 6254
||| |||||
QY 311 -----PheGlyPro-----Gly----- 314
||| |||||
Db 6253 AACACTGAGGGTGTGTAATTC-----CCCCTTCATGGCTTCCAGTAGACTTATAATTCCTCT 6197
||| |||||
QY 315 -----Ala----- 315
||| |||||
Db 6196 TCGATTTCTTCCAAATAATCTGGCAGGCTTTGGAAGAATGGGAGGCTGATAGTGTGAC 6137
||| |||||
QY 316 -----Val-----Ser----- 317
||| |||||
Db 6136 ATCTTGGTCTTATCGTATTTTACCACAGATCAATTTGTGAATTTCTCGGGCTCTGCAAA 6077
||| |||||
QY 317 ----- 317
Db 6076 GGCATCATTTATCTCAAAGCTATTAAAGAACATTGACAGGCTCACTGTAGAAAAACGGCAC 6017
||| |||||
QY 318 -----GluValSer-----Asn----- 321
||| |||||
Db 6016 TTTAATTGGAGAGTACAGCCAGAGAGTCTAGCCCGTCCACTAAGCTCGATACCAATTTT 5957
||| |||||
QY 321 ----- 321
Db 5956 GTCTTTAGTTGTAGGCTTCAAATTTCTGGCTGTATATCTTTGTCAATTCAGGCTGCTCT 5897
||| |||||
QY 322 -----GlyThr----- 323
||| |||||
Db 5896 GAAATTTCCAGCTGTGTGTCTGTTGAGTGGAGTCAAGCAAGGCACAGTGTGTGTCACAG 5837
||| |||||
QY 324 -----Ser----- 324
||| |||||
Db 5836 AGCTGTACTGAGCTGTTCTTTGTACAGGAGATTGTGGCTCGTGGATCTTTGTAGTCAATG 5777
||| |||||
QY 325 Arg-----Arg----- 326
||| |||||
Db 5776 AGAGAAGGTAAAGTGCACAGAGTCTCTGTTTCAACAGAAATTTACTGTATACATCTGCCAGT 5717
||| |||||
QY 327 -----Ala-----Gly----- 328
||| |||||
Db 5716 GTGTTCTCCCGAGAGGGACATTTTCCCATCACCATTGTGTATGTGTGTCGACGCCCAAGGT 5657
||| |||||

VTQMSDLSQVTVHLMASPTENADHCLDPLITKTHLLSSLTVQRNSRNTTEBELS
ARDGPAFHTHOLYLIVDLIRISWTTNTRDIAFLGYDYKKAALVKENLSTEALGLKID
PQMSAKPKRIGIPPSAQYPPHVSTPFSFGPKDGGSGAYMLQKLIETDRFVFTTEE
ESGMSDQCGIAACQTDIDYNNRCLIELVNCQMLRGAETEGCVISAAKQLQCOQH
HPAWYGDTLKOKTSWTKLLDGMQYFAITTESSPTQDQROLWLEVNIBEHRESDSV
QELMESSGOAGVMVTTTTDMQPAQAQAOQVORIISRCNCRMYIISYSHDIDPELAT
QIKPPEVHENOEKEDLLAKQSGAVDTFTLIHLELISNPAQYAMILLIVNNLLHVE
PKRKEHSKKVRQLEISSNPERQSRISILHQEAVRQHVQAQINHLGKQMYISIMKSL
QDQSKNRELLDLNQLQLOQNEKANLQLESEELNILRCFQFOLQRANWELRKOQ
EDVSVRRETFYFAQARWLTTEEDQGLGIAELQRFLYSKVNSDDTAHELHLEIGF
TMNNLLPNAIYKVLRSQSGQQLALRLFVKVRPPVGGISVKEHEFVNVPVLTIO
LSHRFFHMRSGFFPRNVDEDEKSKLVTTGIPVVKPRLIATDDAVPLGSG
KGVAOGLRFSQSVRSFKLPEHPVDDIDMKKERAAMNSRYIKIPQVPLCVSKGE
KNSVDWGLNLVLPCLEYHNNTWTLDFAMAVKRSRKALVAQVIKEKRLKXPATGSE
VNGKLETKCDLNMQQOQEEBKARLLILGLSVGDKNPKKSI FGRRK

ORIGIN

Alignment Scores:

Pred. No.: 1,03e-12 Length: 10481
Score: 1676.80 Matches: 292
Percent Similarity: 10.71% Conservative: 44
Best Local Similarity: 9.31% Mismatches: 6
Query Match: 69.63% Indels: 2795
DB: 11 Gaps: 249

US-10-017-084A-523 (1-344) x AK090138 (1-10481)

QY	1	Met		Lys		Thr		Ile	4
Db	10355	ATGGCGAGCGCTTCTTAATGCCATCTCCCAAGTGAGCACAGACTGGGAAGTTTATC							10296
QY	5							Gln	5
Db	10295	CCCCAAACCAACACCTCTTAGACAACAGGCGTGGAGTGAGGCACAGAGATCAGACT							10236
QY	6	Pro				Lys		Met	8
Db	10235	CCTTCCTTAGCTTATTGGCACAAAGGAGAGCAATTACATTAGAAATATATATATATG							10176
QY	8								8
Db	10175	TTTTATATATATATATCTTTTATAAAATTTATCATATCTTGATCAAAACTATCCCCAAC							10116
QY	9					HieAsn			10
Db	10115	CTTTCGTGTGCCCGAAGACAGGAGTACTAGGCTTGGACAAATCCCTGGGTCTCTGG							10056
QY	10								10
Db	10055	TTTTCTTGCCCTGTGGCCCTGGGTCTAATCCATGAGAGGGAACCCAGCGCTTTGTCCA							9996
QY	11					Ser			11
Db	9995	CCATGCCCTGCAGGGACAGGCCAGCTGTGTAACAATGTCTCAGTTCCTCATATGCCCCA							9936
QY	12	Ile				Ser		TriAlaile	16
Db	9935	CAAACTCTGAGATGAAGGAGGCTCTGCCACCTCAAGTCCCTGG--ATCCTGAGC							9879
QY	17	Phe				Thr			18
Db	9878	CAGAGTCAATTTCTATATCTGTAGTCACTTGGGTCTCCACATCACTTGGCCTGCCGA							9819
QY	19	Gly				Ala			22
Db	9818	GGACTCTTGCCAGGGTCTTGTGCGCCACACATTAAACCAATGAGGAGCGAGCTTTCTC							9759
QY	23					LeuCys		Leu	25
Db	9758	TTCTTCTGCTTGATGTTTCAGGTACACATTTGTTTCTAGCTTTCCCGGACCTCAGA							9699
QY	26					PheGln		Gly	28

Db	9598	CCCCGTGCAGGTTTCAGCCTTAGTTTTTTCTTTGATTACCTGGGCAACGAGACTTTTCG	9639
QY	29	---ValPro	30
Db	9638	GCTGTCCCTTTTGACAGCCATGGCAAAAGTCCAGCCATGTCCACGTGTGTGTGGTACTC	9579
QY	31	---Val-Arg	32
Db	9578	CAGACAGGTTAGCACCAAGTTTAAGGTGCGCCCACTCCACACTGTCTTCTCACCTTATA	9519
QY	32	---	32
Db	9518	ACTGACACACAGTGGAACTTGTGGGATTTTATATATATAGAGGATGTGTTTCATGGCAGC	9459
QY	33	---SerGly	35
Db	9458	TCGCTCTTTTCATCTTGTCAATATCATCAACCTGGGTCTCAGTAAATTTTGGAAATGATCT	9399
QY	36	---AlaThr--PheProLys	40
Db	9398	TCTGACTCCAGAACTCCTGTGTCAAGCCCTGTGCACGCCCTTCCGGAGCCAGTGGTAC	9339
QY	41	---Ala	41
Db	9338	TGCATCATCTGTGTGATATCAGCTGCGAGGCTTTTACAACTGGTATTCAGTAGTCACCAG	9279
QY	42	-MetAsp	43
Db	9278	TTTGACTTATCTCTTTCATCAACCACTTCATCATCTTCTATCATTTTCGACGAGAAAGAA	9219
QY	44	---Val	46
Db	9218	AAAGCCCATCACTTCTATGTAAGAACCGGTGGGACAGCTGGATGTGAGAGCACACATT	9159
QY	47	---Val	47
Db	9158	TACCTCAAAGTGTTCCTTAACAGAGATACCAACAGGTGGCGGACTTTGTGTAAGAG	9099
QY	48	Arg	55
Db	9098	GCGAGGGCTAGCTGTCTCCAGACTGGCAGGAACCTCTGGGGCCTTAGAACCACTTATA	9039
QY	56	ArgCysThr	58
Db	9038	AATAGCATTAGGAGAGGTTGTTCATAGTGAACAGCCCACTCCAGGAGATGTCTGCG	8979
QY	59	-Ile	61
Db	8978	TGTGTCAATCAGATTTATTTCACCTTGTGTAAAGGAACCTCTGTAGTCCAGCTCAGCGAT	8919
QY	62	Arg	63
Db	8918	GCCAGCTGTCCATCTTCTGTGAGCGGCAAGTGCCTGAGCAAGTAATAAATCGGT	8859
QY	63	Thr	67
Db	8858	GCGAGGACCACACTCACATCTCTCTGTGTGTTTTCGAGGCTCCATTTTATGGCTCGCTG	8799
QY	68	Trp	68
Db	8798	CAGTTTGGAAATCTTAAACATCTGATGAGGATGTTCAGTTCTTCGCTTTCCAGCTGCAG	8739
QY	69	Leu	73
Db	8738	GTTCGCCCTTTCTTGGTTCAGCTGTAAGTGTGTTTGGTTCAGTCCAG-CAGATTCT	8680
QY	74	---IleLeu	75
Db	8679	CATTCTTGTGTCATCTCTGTAAGACTTCATGATAGATACATCTGCTTCCCTAGTGCC	8620
QY	76	---TyrAla	77
Db	8619	TTATCTGGGCCACATGCTGCGCACAGGCTCTCTGAGGTGTAGTATGCTGTGCTGCTGCT	8560

QY 77 ----- 77
Db 8559 CCTCAGGATTGCTAGAGATCTCAGCTGGAACTCAGCGCTGTTCTTTTCACTATGCT 8500
QY 77 ----- 77
Db 8499 CCTTCGGCTTGGGTTCTACGTGAGAAAGCAGAGTGTGTGACATGTCCAGAAATCATAGCAT 8440
QY 78 -----Gly---Asn-----Asp-----Lys----- 81
Db 8439 ACTGAGCTGGGTTGGTAGAAATTTCCAATTCGGTGGATGAGAGTAAAGTATCCACAG 8380
QY 82 -----Cys-----Tyr-- 82
Db 8379 CCCCTTCCTGCTTTTAAGAGATCCTCCTTTTCCCTGGTGTCTCATGAACTCAGGTGGCT 8320
QY 83 -----Val----- 83
Db 8319 TAATCTGAGTTGCTAGCTCAGGATCAATGTGATGGCTGTAGCTAATATAGTACATCCGGC 8260
QY 84 -----LeuAsp----- 85
Db 8259 AATTCAACGTGAATGATCCTCTGAGCTTGTCTGGCTTGTCTGGCTTCGGTGGTGGT 8200
QY 86 -----Pro----- 86
Db 8199 TCCAGTCTGGTGTGTGTTAACCATGCTCCCTCCACTGCTGCCCTTCTCCATCAGCTCCT 8140
QY 87 -----ArgVal-----ValLeuLeu----- 91
Db 8139 GAACAGAGTCCAGACTACGTTCCTGGTGTCTCTCAATATTTCTTCACTCTTAACAGAGCT 8080
QY 91 ----- 91
Db 8079 GTCGGCATCCTGTTCACTAGGCTGCTTTCACTGGTGGCAAAATACTGCAATGCCATCTA 8020
QY 92 -----Ser----- 92
Db 8019 ACAGGCAAGTCCAGGAAGTCTTTGTTTCACTGTGTCCATACCAAGCTGGATGTGTT 7960
QY 93 -----Asn----- 93
Db 7959 GGCATGCGACAACTGAGCTTTGGCCAGCGATCAATGACACAGCCTTCTGTCTGTCTC 7900
QY 94 -Thr-----Gln----- 95
Db 7899 CACGAAGAACCATCTGGCAGTTAACCACTCAATAAGGCAGTTCGGTTGTATATGTCAT 7840
QY 96 -----ThrGln----- 97
Db 7839 CTGCTGGCAGGCAAGTATGCCACAAATTTGGTCACTCATACCGGATTCCTCTCTGTGA 7780
QY 98 -Tyr----- 98
Db 7779 ATACTCAAATCTGTCTGTCTTCAATCAGTTCTTGCACATGTAAAGCACTTCTCTGATG 7720
QY 99 -Ser---Ile-----Glu----- 101
Db 7719 ATCCCTTATCAGGCGCTCCACTGAAGCTGGAGTGTGACATGAGTGGGACTTGGGCAC 7660
QY 102 -----Ile----- 102
Db 7659 TAGTGGGATACCCCGCTTTGGCTTTTGGCTGACATCTCAGGATCAATCTTCAAACCTT 7600
QY 103 -Gln----- 103
Db 7599 TCAGGGCCTCAGTAGAGATTAAGTTTGAGTACAGCTGCTTTTTTTGTAGCCATCATATA 7540
QY 104 -----AsnVal----- 105
Db 7539 AGCCAAAGGCATATGCTCCTATTGGTGTGTCGAGGAATCCGTAAATCTACCAATATACA 7480

QY 105 ----- 105
Db 7479 GCTGGTGTATGAAGGAGGAGGATCACCATCTCGAGCAGAAAGCTCCTCTTCACTGGTGC 7420
QY 106 -----Aap----- 106
Db 7419 GATTGCTGTGCGTTGGTAAAGTAAGGGAAGACAGGCTCAATAGGTGGTCTTTGTGATCA 7360
QY 106 ----- 106
Db 7359 AGGATCAAGGAGGAGTGTGAGCGTTCTTCTTCACTGGGTGAAGCCATCAGATGAACAGTCA 7300
QY 107 -----Val----- 107
Db 7299 CCTGACTTAAGTCACTCACCATCTGGTTACTACTCCACTCAGAAATAAGGCGCGCATCA 7240
QY 108 -----Tyr----- 108
Db 7239 CTGTGCCAGCTTGAGGTATAAGCCGCTGAGTTCCCGAGTGAAGACATGCCCTGACTGC 7180
QY 109 -----Asp-----GluGly---Pro-----Tyr----- 113
Db 7179 ACTCAATCTGGAGGCCCTTGTCTGGGCAAGAAAGCCCACTAATGTACTCTGTAGTGGG 7120
QY 114 -----ThrCysSer----- 116
Db 7119 GAAACAGTGCATATAGGAAGCTGTTTGTAGTGTGGCCAAAGTTTTTTCTTGTGGGCT 7060
QY 117 -----Val-----Gln-----ThrAsp-----Asn----- 121
Db 7059 TCAAGTTTATTAACAGATTTTCTCTACAGATAGGCTTGTGTATGTAGTCCAAAGTTGCC 7000
QY 122 -----HisPro----- 123
Db 6999 AGAAATTCGATCCAGCGCAGGTACTACTATACACAGAAATTCGGGCTGGGATATTG 6940
QY 124 -LysThr-----SerArgValHisLeu-----Ile----- 131
Db 6939 TCCCACTATGGCGAGTCAATCCATCTTGATGGAGAGATTGAGTTCTCAGAGCGGAGG 6880
QY 132 -----Val----- 133
Db 6879 CCCGTAGGAGTCAATGAGCTGGCCAGAGGTACCTCAGGCAAGAACTCTGGGCGCCCTCA 6820
QY 133 n-----ValSer-----Pro----- 136
Db 6819 GAGTGACACTGTGATGATCATGAGGATTCCTGGCGCAGCCACTGTAGTCCAGTGTCA 6760
QY 137 -----LysIle-----Val---Glu-----Ile-----Ser---Ser----- 143
Db 6759 TGCAGAGGTCAAGCAGGTCAAGSAGCAGCAGTCTGTACTTCTAGAGGCTGTTCTTACGT 6700
QY 144 -AspIle----- 145
Db 6699 TGACATCCAGTCCCTCTGAAACAAACTGACAGGTTTCCATGAAAGAAAGAGTGGC 6640
QY 146 -----Ser---Ile----- 147
Db 6639 TCCACTCCAGTGCATGTTCTCAGTTGTATTATAGGGTCTCAGTGGCCAGCTGATGCA 6580
QY 148 -----Asn-----Glu----- 149
Db 6579 GGTGTTGCTTTCAATATATCATATGCCAGTCCCATGGAACAGAGACGGCTCTTATGCC 6520
QY 150 -----Gly-----AsnAsnIleSer-----LeuTh 156
Db 6519 ACCAGGCAAGGTGGGCTGGGCTCAGCTGAGAGGCTTAGTCAAGAGGTCCACACACTGAC 6460
QY 156 r-----Cys-----Ile-----Ala----- 159
Db 6459 CAATCAGTGTCCAGGCTGGATCCCAACATGGGCCCCACACCCTGTGTACTGGAAGATT 6400
QY 159 ----- 159

Db 6399 CCGACTGGAAGTCATGGTAAACTTGAAGTGGGGCATGTTCTTCTACTGCCAGTTAC 6340
Qy 160 -----ThrGly----- 161
Db 6339 CCCAGGGAAGCCCAAGTGCAGGATCTGACGTCCAGCGGAGCATGGCTGGCCACTCTGCT 6280
Qy 162 -----Arg----- 162
Db 6279 CAGTCCCGCAAGTCAGCCATTAGCCCGCAGTCCCGGATCTCAACAGGTACCGTGGAT 6220
Qy 163 -----Pro-----Glu----- 164
Db 6219 AGTCTCTGATCGAACCAGAAAAGTTTTCACATTGCACTTGAGCATACGACACCACTGAG 6160
Qy 164 ----- 164
Db 6159 TGACAAGATCCATTCCTTCAGCAGGAAAAGGGCTTCCAGGATCAAGTTCTCGAACCTGCT 6100
Qy 164 ----- 164
Db 6099 CTATCATGCTCGGGCCCATGAAGGATGCATCTGTAGAGCCACCAAGCTCTAGCCCTG 6040
Qy 165 -----Pro-----Thr-----Val----- 168
Db 6039 CCAGGCTCCAAAGTAGCAGTCACCGCGCATGGGTGTGTGCCATAGAGACGACGAGAGC 5980
Qy 168 ----- 168
Db 5979 GCTGATGATAGATTTCAATGTTTTTGGGTTCMAAGAGCGGTAGAGCTCCCAATTTTCC 5920
Qy 169 -----TrpArg-----His-----Ile----- 172
Db 5919 GAGCTGGCAATAGCTCTCCATGCTCTTCGAGGCGAGCCACTTTGGCACTAGCAACT 5860
Qy 173 -----Ser----- 173
Db 5859 GCAGCCTTTTGGCACTCTCTTACTTTCATCTTCATCCTTCATCAGTTCTGTTATCATGAAGTT 5800
Qy 174 -----Pro-----LysAla-----Val 177
Db 5799 TCACCTCAAGATGTCATCCAGGAAAACCAAGAAAAGTCTGAACCTTTTAGGAGTAAT 5740
Qy 177 l-----Gly----- 178
Db 5739 CAGGTGGAAGAGGGCGAGGGCTTGGAGAAGCCCAAGCATGAGTCCCTCGATCGAGCCCT 5680
Qy 179 -----Phe-----Val-----Ser-----Glu----- 182
Db 5679 TTAGCAATTTGAACTCCACAGCCTCATCCAGAGTTCGAGAGAAGTCACTACTGATAAG 5620
Qy 183 -----Asp----- 183
Db 5619 GAAACTCCACTGAGACTGATCCGAGGAAAGAACCAACCGATTCGAGGGTCTGCA 5560
Qy 184 -----Glu----- 184
Db 5559 GCGCAGGGAAGGGTTCTCTGTGAAGGATCATCTTCTAGCTCAGGCAAGCTGCACCT 5500
Qy 185 -TyrLeu-----Glu-----Ile-----Gln-----Gly-----I 191
Db 5499 CTACCTCTTCAAGTTGAAGATGCTATTCCTCATCAAGCCAGCAGCAACTCGGGGAGT 5440
Qy 191 e-----Thr-----Arg----- 193
Db 5439 AAGCCTGCAGTGAACCTCCATGCGGTTTCAGCGACACACTCTCTGAGCCAGGTAATGA 5380
Qy 194 ----- 194
Db 5379 ACTGTCTCAGCCAGAAAAGTGTGTAGCTTGGAGTGTCTACCTCCAGGGTCAGGGTGA 5320
Qy 194 uGln----- 195

Db 5319 GCAGCCGCTAGGCAGGATGACTCAGGGAGATGGTCTTCTGGCTCCCAAGTGGACTGTG 5260
Qy 195 ----- 195
Db 5259 GAGTGTTTAGTGAATGGGACTCAATAATCTCAGGAAAACACAGTAGTCTCGTAAGAGGTCTC 5200
Qy 196 -----SerGly-----Asp-----Tyr-----G 200
Db 5199 GGCACCTAGAGTGGCCCTGACATGTTGGTACAGATACATGTGATCTGGGGGGTCCAGA 5140
Qy 200 u-----CysSerAlaSer-----Asn----- 205
Db 5139 GTAAAGTCAGCCCTGCACC-----ACACTGAACCTCTAGAGAGCGATGCTGTGTGATAG 5083
Qy 206 -----AlaAla-----AspVal----- 209
Db 5082 TGAGGGAGATGGAGAGAGCCAGCACTGGCGTGGGGATGTACAGGAGCCTTGCACAGG 5023
Qy 210 -----Pro----- 210
Db 5022 GCTGCATCTTCTGTGACTGATTTTACTAATGCAAGCACAGTCTTGAATCCCCAG 4963
Qy 210 ----- 210
Db 4962 TGGAGGTCTCAGCACTACCAAGACAGTCAGTGTGTCCAGTCTGTAGTCTTGAAGCACC 4903
Qy 211 -----Val-----Val----- 212
Db 4902 CCAGTGGGAAGAGTGAACAGGTTTCATGTTCCACCTTCAAGTCCACCTTCCACAGTA 4843
Qy 213 -----Arg----- 213
Db 4842 AGGTACAGACTCCCAAGTGAAGCTCTCTAGAGACAGCTGACCTTTCAGATTGTGAA 4783
Qy 214 -----Arg----- 214
Db 4782 TCACAAAGAGAGAGACTCGAGACAGACACTGGGCACAGATGTCTGATATTCTTACCTGAA 4723
Qy 215 -----Vallys----- 216
Db 4722 GTCTCTGANTAGTACAGTCAAGAAAAGATTTGGACTGGTGGTCTGGACAGCCAGGG 4663
Qy 217 -----ValThr----- 218
Db 4662 GCTGGTTATAACTTCTCTGTAGTGTGAAGGAATCCAGAACAAAGTGTCTGCCCCAACAT 4603
Qy 219 -----Val-----Asn----- 220
Db 4602 GCATATTAGGTGGATGTGTGTCGCCGCTGAATGTGGAGTCACTGCCACAGCCAGCAGA 4543
Qy 221 -----Tyr-----Pro----- 222
Db 4542 GATGATCTTACAGTTAGCACTGCTCGTATGATGATACTTTTGTGGCCGAGGTGCTGTAGT 4483
Qy 223 -----Pro-----Tyr-----IleSerGlu----- 227
Db 4482 CCAGGAGATGGAATTGAACCCCAAGCAACCGTGTGTATCTCCAAGCTGAATGGA 4423
Qy 228 -----AlaLys-----Gly----- 230
Db 4422 TGCTGACATTGGAGACTGAGGTGTGAAGATAATGGGAGCCAGGATCTGAGGGAGGTTC 4363
Qy 231 -----Thr-----GlyVal----- 233
Db 4362 TTTTCTTTCTTTTAAAGATCAGGTGAACCTGCTCTTGGGTCTTCCAGTCTTAGCATAA 4303
Qy 234 -----ProVal-----Gly-----Gln----- 237
Db 4302 GGAGCCAGTGAAGAGAACTCTTGGTTCGGTAAATGAATGATACAGGTGTTCAGAACTAG 4243
Qy 238 -----LysGly----- 239
Db 4242 AAGCTGAGAGGTGATGTGTGTCACCTGCACATTTAGCCCTTGAGGGAGTTGAGGCAGCAA 4183

QY 240 -----ThrLeu-----Gln----- 242
Db 4182 TTGTTGGGCACTCTGGACAGCAACACCCATCTTCCATAGAGTTCAGTCTCATCT 4123
QY 243 -----CysGluAlaSer-----AlaVa 248
Db 4122 GTGCCATATCATAGTTTGTCTGTAAGCTTCGAAGCGGCACTGGTCTCATCAGGTGGT 4063
QY 248 1-----ProSerAla----- 251
Db 4062 ACAGGAATGCACAGCTTCAGTGTCCAGTCAAGTCCGCTTTTTCAGTGTTCATAGACA 4003
QY 252 -----Glu----- 252
Db 4002 ACACCACACTGTGTCTCCATCTTCACCTTGACTTGGTCTGCGACCGCTGGAGGAGGT 3943
QY 253 -----Phe-----Gln----- 254
Db 3942 ATAGCCAGGACAGAGTTGGTTTCAGCAAAGTTCTCAGTCAAATCTGAACAGAACTGATT 3883
QY 255 -----Tyr----- 255
Db 3882 TGGAAATCCGGCTTGGGATGACACAGTAGCTGATATGGAAGAGACCTTCATGCAGCT 3823
QY 255 ----- 255
Db 3822 CAGCATGGAGTGTCCACACATCCACAGTGACAGCCGTGAGTCCCAACTGCTGACGCTGA 3763
QY 256 -----Tyr----- 256
Db 3762 CCTGTAGGCGCAGGTCGAGGCGCAGTGAGAGCTCTACAGACATGTATCTCCAGCTGAC 3703
QY 256 ----- 256
Db 3702 CACTCTTCAGGACTTCGCTATTGATCTTTGATAGTTCATTTACATGATGAGACTCTTCC 3643
QY 257 -----Lys-----Asp-----Lys-----Arg----- 261
Db 3642 CATCACTGTCCAAAGAAATCTGCTTCTACTGATCTGGATGTGCCACAGGACTCAGAGG 3583
QY 262 -----Leu-----Ile----- 263
Db 3582 TAGCCACCTTAAGAACCATTGATTTATGGCATCTACATGAATGGAGAAATAGTTGGCAGA 3523
QY 264 -----GluGly----- 265
Db 3522 AGATCTTCAACAGGATGGGCTGAGGAGCAGTTCTCTTTTGCTCCACTCTGTGTCTGAG 3463
QY 266 -----Lys----- 266
Db 3462 AGAATGGGCGACAGAGCTAGAAACCTTCTGTAGATCTGTCTGTATGCGCACTTCTCCAA 3403
QY 266 s-----Lys-----Gly----- 268
Db 3402 AGCACAATGCCCATAGTTTGGCAGATCATGGCTAAGGAGTTTGTGGAAATCCACAAGT 3343
QY 269 -----Val-----Lys-----Val----- 271
Db 3342 TGTCAATTTCCACCGTCTGTGTCTGTCTGCTGAACTTAAAGACTGACATCTCTGGATCCAA 3283
QY 271 ----- 271
Db 3282 AAAATCGAAGGAGCCAATCTTTAGCTCTGCTGCAACTTGGCTGACACACCTGGTGG 3223
QY 272 -----Glu----- 272
Db 3222 CCNACCGGACCAAGCCACCGGCTAGGAAGAGTGCCTAAGCGCAACCCAGCAGCAAGA 3163
QY 272 ----- 272
Db 3162 CCAACAGCGCGGAGAGAAATAGAGGCAATTTAGTTCGGGTCCGGCCCGGCGCTGGCCCGCA 3103

QY 273 -----AsnArgPro-----Phe----- 276
Db 3102 CCCCCGCCATGCGGGCCCTGACGCGGAACCGCCCGCTCTCGAGTCTCTGTGGAAGTTG 3043
QY 277 ----- 277
Db 3042 ATGTTTTCATATTTAGTGGCCATTCCTATTCTCTCTTTTGTGAATGCGCTTTTATATCCT 2983
QY 277 u-----Ser----- 278
Db 2982 TGTCTCTCTTATTTTGAATGTTTCTTATTATTGTGAAGAGTTTCCCATCTAACCTTA 2923
QY 279 -----Lys----- 280
Db 2922 ATTTCTAAATCTTATTGTTTATATTATACAGATGCATCCAGCATGTGCTGTGTTTT 2863
QY 280 uile----- 281
Db 2862 AATTTGTAGTGGGCGCACATGCGGTTAAAAATTTCCCTTCTATTACTAAATCTTTAGG 2803
QY 281 ----- 281
Db 2802 GATTTTCATTTCCAATATCAAAATAATTPAATGGTTATAAATCTACTTAGTTTTCTATT 2743
QY 281 ----- 281
Db 2742 TCTTCTTGAGTTACTTTTGGTAGTATATGTTTTCAATCAAAATGTTCTACTTTTAA 2683
QY 282 -----PhePheAsn----- 284
Db 2682 GTTTAAATTTTATGGCTTAAATTTGACTTAATCTTAATCTTAATTTTAAATTTCTA 2623
QY 285 -----ValSer----- 286
Db 2622 CTTTATCTCCAGCATGTCTCTCTTTTAAATCTCTCTATATTGAAATTTATTAGTCTCT 2563
QY 287 -----Glu-----His----- 288
Db 2562 ATTGTGGCTATAGAATAATACCACAAATCAGTGGCTTAAACACGACACATTTATTATT 2503
QY 289 -----Asp----- 289
Db 2502 TTGCAATCTCGAGATCTTAATCCAAATCAGTTTCTCACTGGACTAAAGTCAAGGTACCA 2443
QY 290 -----TyrGly----- 291
Db 2442 GCAGGTCTGAGTTCCTTCTGGTGGCTATGGGAATAATCTGTCTTTTCTTTTCTTTT 2383
QY 292 -----Asn----- 292
Db 2382 TTTTGTGCTTTTCCAACTTCGAGGCTGTTCTCATTTCTCTCATCATGCTTTCTTTC 2323
QY 293 -----Tyr----- 293
Db 2322 ATTCAGTCTACTGCTCTCCCTTTTATAGATCCTTGTGATTCCTCACTGGGTCTGCTGG 2263
QY 294 -----ThrCys----- 295
Db 2262 ATAAATTGAGGATAAATCTTCTCATTTCAAGATTTTGTGAATTAATCATGTATGTAAGTTT 2203
QY 296 -----ValAlaSer-----Asn-----Lys----- 300
Db 2202 CTTTCACTATATGTTTGGTTAAATTTGATATCCCGGAGAAATTCATATGTTGAAGTTCT 2143
QY 301 -----LeuGly----- 302
Db 2142 AACCTTAGGTAGGACGACAGCAATCAGCCCGGAGGATTTCTGGGAGAGAGCGGTCCA 2083
QY 302 ----- 302
Db 2082 GGAGAGAGATGGGACATGTCTCTTTTCTGCTCTTATAGATTACAGAGCAAGATTCGTCA 2023
QY 303 -----His-----Thr-----Asn----- 305

Db 2022 ACTCCATAATAGCAGCAGAACTCTTTGTTTCAGTGTGTATCCCTAGTGCCTTAGA 1963
QY 306 -----Ala-----Ser-----Ile----- 308
Db 1962 ACTGTGCTTGGCACAATAATACATGCTCAGTAATAATTTGTAGAAATGAGAAAAGCTTTCAA 1903
QY 309 -----Met-----Leu----- 310
Db 1902 GGCCATGCTGTGCTGTCTTTCGAGAGAAGTTGAGATAAGCTCTCCGCTCCATCGAGTCA 1843
QY 311 -----PheGly----- 312
Db 1842 GGATGCTTTTGGGGTGTCTGTGGGTGAGGAGTAGTCTGTAAGACTCAGGTTAGGATC 1783
QY 313 -----ProGly----- 314
Db 1782 GTTGTGCTCCCTGAAGAGGTTTAACCTTTGCCAAACAATCCGGGAAGCAACAGAAACCCCG 1723
QY 315 -----Val----- 318
Db 1722 GGCAGAACTGTGAGGAAGAAAGATGTGATCAGAGAAATATTGCTCTGAAGAGAGAC 1663
QY 319 -----ValSer-----Asn----- 321
Db 1662 AAAAATCAAGCTGAGGGTCTGGGAGTCACAGATGGGATGGCTCTCCAGACAATCATTTG 1603
QY 322 -----Gly----- 322
Db 1602 AAGACCAGACCCCTGGGATCGGACAAAGACGCTCACCGAGCTAGGACCTAGAACCTCC 1543
QY 323 -----Thr----- 323
Db 1542 AGTGGGCTCGGAGCGGACAGCGGTGCTCTCCACTCCCTTAACCGGGAGGGTG 1483
QY 324 -----SerArg----- 325
Db 1482 GAGGCTCAGGAATGTGTGATTTATGCTAGTACAGGAGTGCACAACTCATACATTGAG 1423
QY 326 -----AlaGly----- 328
Db 1422 GGAGAAAGCAGCGGAGACGCGCACAGATTCGCCCATCTCTTTGAATAFAATTTTGA 1363
QY 329 -----CysVal----- 330
Db 1362 TTGAGATTCAATTAATCCGAGGGGAAAACATTTATGAGGCTGAAGCTGTCTCGTTG 1303
QY 331 -----Trp----- 331
Db 1302 CCAGAGACAGGTTATGAGCTATCAATGCAATTACATTAAGACAGATTAATCTGGGCAA 1243
QY 331 ----- 331
Db 1242 ATTGAGCAATTAGAGGTGAGATCAAGAAACGGCTCTGATCTCTTTTCCCTCTTCT 1183
QY 332 --Leu--LeuProLeu-----Leu----- 336
Db 1182 CTCTCCCTCTCCCTCTCTCTCTAAATGCAAGTTCGTAGTCTCTTCCAAATTCGGAGGCACA 1123
QY 337 -----ValLeuHis----- 340
Db 1122 AAAGTAGGTGAGACTGCTTTTGTATCTCGGAAGTCTTCACTCTCTGATGTAATTTAGC 1063
QY 340 eu-----Leu-----Leu----- 342
Db 1062 TGAGTGCAATCTAGGTTAAGACCGGACAGCGGTAATTAGAGCCCTAGCTGCCGGA 1003
QY 343 -----Lys-----Phe 344
Db 1002 GGACCGCGCGCCCGCCAAAGCGCGCCCGAGTCGGCGCCCTTC 959

RESULT 22
AK090138

LOCUS AK090138 10481 bp mRNA linear HTC 20-SEP-2003
DEFINITION Mus musculus 7 days embryo nullipotent stem cell CRL-2070 NE cDNA,
RIKEN full-length enriched library, clone:G431005B01 product:gene
e1 protein, full insert sequence.
ACCESSION AK090138
VERSION AK090138.1 GI:26354968
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Mech. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Hayada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 120481
PUBMED 120481
REFERENCE 6
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tanaka, M., Tagawa, A., Takahashi, F., Takaku-Akai, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>
URL: <http://fantom.gsc.riken.go.jp/>

FEATURES

source

```
1. 10481
   /organism="Mus musculus"
   /mol_type="mRNA"
   /strain="C3H/J"
   /db_xref="PANTOM,DB:G431005B01"
   /db_xref="MGI:2429044"
   /db_xref="taxon:10090"
   /clone="G431005B01"
   /cell_line="CRL-2070 NE"
   /cell_type="nullipotent stem cell"
   /clone_lib="RIKEN full-length enriched mouse cDNA library"
   /dev_stage="7 days embryo"
   /notes="unnamed protein product; gene e1 protein
   (PIR|S48861, evidence: FASTY, 99.9%ID, 100%length,
   match=3565)
   putative"
   /codon_start=1
   /protein_id="BAC41111.1"
   /db_xref="GI:26354969"
   /translation="MPLFSAIIVLVLLVALSLFLGRMLVRLVRLATRWCKQLQAEIKI
   GSPRFQIWNVSILFOHOQTVEIDNLWISSLLKSHLDLNYVALCPGEVRIETDLQKV
   SLSAPFSONTEVEQKELSLSPSLKIFQLPSIHVDAINIMVLKVATSESLWHQIS
   RSRFLDSGKSLIKVNLKINSKINSEVLKSGLEDICLVELSLALDURLQVSVSSWHLT
   AVTVQWNTLHAEHLGFHSQLLCHAPRISKSVSCSDLTENPAEPTLPGLLQRLP
   LLELGLLSQSQRIVCLNLSKANYQVTTIDLSASLVNTCTIHYRHOBFHMLML
   ALETQASPDQKQRKRPFPQIAPIFSTSVSNVSIQIGDTPPEALGENSISLD
   YOHLRQSIHQRAVLTVHLCWVGSDSHIQRAHPNPMHVMGEALVLSFTLQGSYN
   QPLGLSTQNTLFLCTIRGLQVEISDICACLSRLVLSIVPQSRSAVSRKSGE
   SVTLVLDLQEDMELFTLSALVGASELRLDTLVLSAETSTVGIQGLVLAIVKSV
   TEMQCCPKADPTPVLGLSMLSTYHSISLEVCQAGLTLMLSPDPHMYLYOHV
   RATLQCDLRLATVPEIIEHSNLTPOSTWEPEDHLPESLPRLLTLTLEVTAKL
   TAFVARDKFTLAAESVSLNRHGGSLQAVPELAAGFDGNSIFNLKEVSVQLLPLEE
   MILNRSPALOTLRNRWLLSLGSVSVFFQYDPSRTLDEAVGVQKWLKLRGTH
   AWASPPALPPELLLKVQHSWFVLDLIFEVLHONYELMKDESKEAKRLQLLOAK
   VALRQKHELPAKIEELIYASERKNIEIYIORSRRLYGNTPMRALLTWLSLAGE
   LVALADSLFGPHEVIEQRELDPGSPFFAEGMDIVTQWCRMLKCNKVTFLVIRDP
   RYLFEDRWLRAGTQSGQSCRRRQILHLGFWGNAVVRNMPFLKFYHDFHS
   EIFQYTVWGPCWDPAWTLIGQCVDLITKPSADSPPLPMWDKSRLLFTGDMHMDIEQ
   ANLHQLATEDPYNTTENNWEWSHLSPHMKPGQVFRGDLVNVRTASXYDDCCFLHL
   PDLCTLIDLQMLCHGNPHDHSVTLRAPELPEVPLGQLHDSYRAFSENLNLSIKMD
   LTRHSGTISQPRILVYSSTLRWNQFWATWTSITRPICRGLFNNLKPCKKQKQHYK
   QLSYALFFPOLQVHYWASFAQQRGIQIECSQGHVFRGTORLIPQATGVMRRLISEWS
   VTQMSDLQSVTVHLMASPTENADHCLDPLITKLHLLSSLYTQRHNRITTEELS
   ARDGDPAFTHQLYLDLRLISWTTNRDIAFLGYDGYKAAVLRNLSTALKGLKID
   POMSARKPKRGIPESAQVPVPHVSTPFGSRPDKSGSGGAYMLQKLTETDRFVFTEE
   ESGMSDQGLGACQDIDDYNRNCLIELVNCOMVLRAETEGCVIVYSAKAQLQCOH
   HPWYGDTLKQKTSWCLLDGMQYFAITSSPTEQGRQLNLEVKNIIEHRSLDSV
   QELMESQAVQGVWTTTDMNQPAEQAOQQVRIISRCNRMYYISYSHDIDPELAT
   QIKPEVHENQEDKLLKQEGAVDTFTLHLEISTNPQAVAMILDIVNNLLHVE
   PKRKEHKKQRVRFQLETSNPEORSITLHQEAVRQVQVIRHLGHWMSIMKSL
   QDDKNENLLDLQKLOLNOEKANOLESEELNILIRCFKDFOLQRANKMELRQKQ
   EDVSVVRRTFEYFAQARWLTETEDQGLGIAELQRLFLYSKUNKSDTAEHLLLELWF
   TNNLLPNALIKVVLVPSQSCQGRQLALRFLSKVRPPVGGISVKHFEVNVVPLTIQ
   LSHRFFRHMGGYFFRGNVEDVEDEKSLVTGIPVVKPRQLIATDDAVPLGSG
   KGVAQGLTSSGVRFRKLPPEHVDIDDKMRKAAMNNSFYIKIPQVPLCVSYKGE
   KNSVMDGLNLVLPCLIEYHNNTWLDLFAMAVKRDKRKALVAQVIEKRLRLKLPATGSE
   VRGKLETKCDLNLNQVEEEKARLLIGLSVGDKNPKGKSIIFGRK"
```

CDS

```
DB: 11 Gaps: 248
US-10-017-084A-523 (1-344) x AK090138 (1-10481)
QY 1 MetLysThr---Ile-----Gln 5
   ::::|||||
Db 1145 CTACGAACCTGCAATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCAG 1204
   ::::-----Pro-----Lys----- 7
QY 6
Db 1205 AGCCGTTTCTTGAATTCACCTCTTAATGGCTCAATTTGCCCACTATAATCTGTCTTA 1264
   ::::-----Hisen-----Ser--- 11
QY 8 Met
   ::::|||||
Db 1265 ATGTAATTCATTTGATAGCTCATACCTGTCTCTGGCAACACACACAGCTTTCACCTC 1324
   ::::-----Ser----- 13
QY 12 Ile
   ::::|||||
Db 1325 ATAAAGTGTTCCTCCCTCGGATTTAATCTGAATCTCAATCTAAATATATATTCAAAGAG 1384
   ::::-----AlaIle----- 16
QY 14 Trp
   ::::|||||
Db 1385 TGGGGGAATCTCGTGCCCGCTCTCCCGCTGCTTCTCCCTCAATGATGAGGTTTGCACT 1444
   ::::-----Phe----- 17
QY 17
Db 1445 CCTGCTACTGATAAATGCACACATTTCTGAGGCCTCCACCCTCCCGGTTAATGGGA 1504
   ::::-----Thr---Gly-----Leu---AlaIle--- 22
QY 18
   ::::|||||
Db 1505 GTGGAGACACACGGCTGTCCGGCTCCGAGCGCCACCTGGAGGCTTCTAGGTCCTAGCTC 1564
   ::::-----LeuCys----- 24
QY 23
   ::::|||||
Db 1565 GGTGAGCGTCTTGTCTCCGATCCAGGTCGTGGTCTTCAATGATTGTCTGGAGGAGCGA 1624
   ::::-----Leu-----Phe-----Gln----- 27
QY 25
   ::::|||||
Db 1625 TCCCATCTCTCACTCCAGACCTCAGCCTTGATTTTGTCTCTTCTTCAGAGCAATATT 1684
   ::::-----Gly----- 28
QY 28
   ::::|||||
Db 1685 TCTCTGATCACATCCTTTTCTTCTTACAGTTCTGCCCCGGGTTTCGTGTTGCTTCCCG 1744
   ::::----- 28
QY 28
   ::::|||||
Db 1745 GATTGTTGGCAAGTTAAACCTCTCTCAGGCGACAAACGATCCTACCTGAGTCTTACAG 1804
   ::::----- 28
QY 28
   ::::|||||
Db 1805 CACTACTCCTGACCCCGACGACGACCCCAAGCATCTCTGACTCCATGCGAGCGGAGAGC 1864
   ::::----- 28
QY 28
   ::::|||||
Db 1865 TTATCTCAACTTCTCTCGAAGCAAGCAGGCGATGGCCCTTGAAGCTTTTCTCAITCTAC 1924
   ::::-----ValPro-----Val---Arg----- 32
QY 29
   ::::|||||
Db 1925 AAATATTTACTGAGCATGTATTATGTGCGCAAGCAGACAGTCTTAAGGCATAGGGATACAGC 1984
   ::::-----Ser-----Gly-----Asp----- 35
QY 33
   ::::|||||
Db 1985 ACTGAACAAAAAAGAGATTCCTGCTGCTATTATGAGATTGACGATCTTCTGCTCTGTAAC 2044
   ::::-----Thr----- 40
QY 36
   ::::|||||
Db 2045 CATAGGCGAGAAAGAGAGAGATGTCCTCTTCTCTGAGCCCTGCTTCTCCCCAGAA 2104
   ::::-----Ala----- 43
QY 41 Ala
   ::::|||||
Db 2105 TCGTGGGCTGATGTTCTGGCTGCCCTACCTAGAGGTTAGAACTTCAACATATGAATTTT 2164
   ::::-----Asn---ValThrVal-----Arg----- 48
QY 44
```

ORIGIN

Alignment Scores:

Pred. No.:	1,09e-12	Length:	10481
Score:	1675.40	Matches:	289
Percent Similarity:	11.11%	Conservative:	45
Best Local Similarity:	9.61%	Mismatches:	6
Query Match:	69.58%	Indels:	2667

Db	2165	CTGGGATACAATTAAACCGAATAACATATAGTGAAGAAGAACTTTTACATCATGATTAAT	2224
QY	48	: : :	48
Db	2225	TCAAAAATCTTGAATGAGAAGATTATCTCTCAATTATCCAGGCAGACCCAGTGGAAATCA	2284
QY	49	GlnGly-----GluSer-----	52
Db	2285	CAAGGATCTCTATAAAGGGAGGCAGTAGACTCTCGAATGAAGAAGAAAGCAATGTGATGAGA	2344
QY	52		52
Db	2345	GAATGAGAACAGCCTCGAAGTTGGAAATGGCAAAAAAAGAAAAAAGAAAAAAGAGACAG	2404
QY	53	-----Ala-----Thr-----	54
Db	2405	ATTATTCCCATAGCCACGAGAACTCAGACCTCTGCTGTACTTTGACTCTTTAGTCCAG	2464
QY	55	-----LeuArg-----Cys-----	57
Db	2465	TGAACTGATTTGGATTTAAGATCTCCAGATTCCAAATTAATAATGTGCTGTGTTTT	2524
QY	58	-----ThrIle-----Asp-----	60
Db	2525	AAGCCACTGATTTTGTGTAATTTCTTATAGCCCAATAGGAGACTAATAAATTCATAAA	2584
QY	60	-----	60
Db	2585	TAGGAGAGATTAAAGAGGACATGTCCTGGAGATAAAGTAGAATTAATAAAAAAATTAGC	2644
QY	61	-----Asn-----Arg-----	62
Db	2645	ATAAGTTAAGTACAAATTTAAGCCAAATAAATTTTAAAACTTTAAAAAGTAGAACAATTCG	2704
QY	63	-----ValThr-----Arg-----	65
Db	2705	AATGAAAAACATATACTACCAAAGTAACTCAAGAGAAATAGAAAAACTAAGTAGATTT	2764
QY	66	ValAla-----Trp-----Leu-----	69
Db	2765	ATAACCATTAATTTATTGTGATAATTGGAATGAAAAATCCCTTAAGATTTAGTAATAGAG	2824
QY	70	-----Asn-----Arg-----	71
Db	2825	GGAAATTTTAACTGTCATGTGCGCCCACTACAAAATTAATAAACAGACACATGCTGGAT	2884
QY	72	-----Ser-----Thr-----IleLeu-----	75
Db	2885	GCATCTGTAAATAATATAACCAATAAGATTTTAGAAATTAAGTTAGTGGGAACTCTT	2944
QY	76	-----Tyr-----	76
Db	2945	ACAAATAATAAGAAAAATTCAAAAATAAGAGAGACAGGATATAAAGGCAATTCAAA	3004
QY	76	-----	76
Db	3005	AAGAAGAAATAGGAATGGCCACTAAATATGTAAAAACATCACTTCCACGAATCTCGAGAG	3064
QY	77	-----AlaGly-----	78
Db	3065	CGGGCGGTTCGGCGTCAGGGCCCGGCATGGCGGGGTTCGGGCCAGGCCGGCCGGAC	3124
QY	79	-----Asn-----	79
Db	3125	CCGACCTAAATGGCTCTATTTCCTCCGGCGCTTGGCTGTGCTGTGCTGGCTTAG	3184
QY	79	-----	79
Db	3185	CGCACTCTCTAGGCCGTTGGCTTGTGGTCCGTTGGCCACCAGGTGGTGTGAGCGCAA	3244
QY	80	-----AspLysTrp-----Cys-----	83

QY 125 -----ThrSer----- 126
 Db 4382 GGCTCCCATATATCTTCAGCACCTCAGTCTCAAATGTCAGCATTTCCATTGAGTTGGAGA 4441
 QY 126 ----- 126
 Db 4442 TACACCACCGTTTGTCTTTGGGGTTCAATTCATCTCCCTGGACTPACCAGCACCTCCGGCC 4501
 QY 127 -----Arg-----Val--HisLeu-----Ile----- 131
 Db 4502 ACAAGATATCATCAGCAGCAGAGTGCTAACTGTAGATCATCTCTGCTGGCGTGTGGCAG 4561
 QY 132 -----ValGln----- 133
 Db 4562 TGAATCCCATATCAGCGGGCACCACATCCACCTAATATGCATGTTTGGGGCGAGCACT 4621
 QY 134 -Val-----Ser-----Pro----- 136
 Db 4622 TGTTCGTGATTCCTTCACACTACAGGGAAGTTATAACAGCCCTGGGGCTTGTCCAGCAC 4681
 QY 137 -----LysIle-----ValGluIleSerSe 143
 Db 4682 CCAGTCCAAATACTCTTTCTTGACTGTACTATTCGAGGACTTCAGGTAGAAATA---TC 4738
 QY 143 rAspIle-----Ser-----Ile----- 147
 Db 4739 AGACATCTGTGCCAGGTGTCTGTCTCGAGTCCCTCTCTCTGGTGTATCCACAATCTGAAAG 4798
 QY 147 ----- 147
 Db 4799 GTGAGCTGTCTTAGGAAGTGTCACTTGGGGAGTCTGTGACCTTACTGTGGAAGTCTGA 4858
 QY 148 -----Asn-----Glu-- 149
 Db 4859 CTTGAAGGTGGAAGACATGAACCTGTTCACCTCTTTCGGCACTGGTGGTGCCTTCAGAGCT 4918
 QY 150 -----Gly-----Asn--AsnIle----- 153
 Db 4919 ACGACTGGACACACTGACTGTCTTGGGTAGTGTGAGACTCCACTGTGGGGATTCAGG 4978
 QY 154 -----SerLeuThr-----Cys----- 157
 Db 4979 ACTTGTGCTTGCATTAGTAAATAGTCAAGTCAACAGAGAAGATGACGCCCTGTGTCAAGGCTCC 5038
 QY 158 -----IleAlaThr-----Gly----- 161
 Db 5039 TGACATCCCAACGCCAGTGTGGGTCTCTCCATGCTCTCCCTCACCTATCAGACAGCAT 5098
 QY 162 -Arg-----ProGluPro-- 165
 Db 5099 CCCTCTCTAGAGTTTCAGTGTGTGGTGGAGGGCTGACTTTTACTCTGGAGCCCC--CCAGA 5155
 QY 165 ----- 165
 Db 5156 TCACATGTATCTGTACAACATGTCAAGGGCCACTCTACAGTCCGAGACCTCTTACGAGC 5215
 QY 166 -ThrVal-----ThrTrp-- 169
 Db 5216 TACTGTGTTTCTGAGATTATTGAGTCCCATTCCTAAACACTCCACAGTCCACTTTGGGA 5275
 QY 169 ----- 169
 Db 5276 GCCAGAAGACCATCTCCCTGAGTCACTCCCTGCTAGCGGCTGTCTCACCTGTACCCCTGGA 5335
 QY 169 ----- 169
 Db 5336 GGTGAGCACTGCCAAGCTAACAGCTTTTCGTGGCTGAGGACAAGTTTCAATCCCTGCTGC 5395
 QY 170 -----ArgHis----- 171
 Db 5396 AGAGAGTGTGTGCTGAACGGGATGAGGTTTCATGTCAGGCTTACTGTCCCGAGTTGGC 5455

QY 171 ----- 171
 Db 5456 TGCTGGCTTTGATGGCAATAGCATCTTCAACTTTGAAGAGGTAGAGGTGAGCTTCTGCC 5515
 QY 172 -----Ile----- 172
 Db 5516 TGAGCTAGAAGAGATGATCCTTCCACAGGAACCCCTTCCCTGCGCTGCAGACCCCTCCGCAA 5575
 QY 173 -----Ser-----Pro----- 174
 Db 5576 TCGGGTTTGGCTTCTTTCCCTCGGATCAGTCTCAGTGGAGTTTCTTATCAGTATGACTT 5635
 QY 175 -----LysAlaValGly----- 178
 Db 5636 CTCTCGAACTCTGATGAGGCTGTGGAGGTTCAAGAAATGGCTAAAGGGGCTGCATCGAGG 5695
 QY 178 ----- 178
 Db 5696 GACTCATGCTTGGGCTTCTCCAAGCCCTGCCCTCTTCCACCTGATTTACTCCTAAAGGT 5755
 QY 179 -----Phe--Val----- 180
 Db 5756 TCAGCACTTTTCTTGGGTTTTCTCGATGACATCTTTGAGGTGAAAATTCATGATAACTA 5815
 QY 181 -----Ser--Glu-----Asp----- 183
 Db 5816 CGAACTGATGAAGGATGAAGATGAGGAGTGCCTAAAGGCTGCAGTTGCTAGATGCCAA 5875
 QY 184 -----Glu-- 184
 Db 5876 AGTGGCTGCCCTGCGAAAGCAGCATGGAGAGCTATTGCCAGCTCGGAAATTCAGGAGCT 5935
 QY 185 -Tyr-----LeuGlu-----IleGln----- 189
 Db 5936 CTACGCTCTTTTGGAAACGCAAAAACATTTGAAATCTATATCCAGCGCTCTCGTCTCTA 5995
 QY 189 ----- 189
 Db 5996 TGGCAACACACCCATGCGCGGTGCACTGCTACTTGGAGCCTGGCAGGCTAGAGTGGT 6055
 QY 190 -----Gly-----Ile----- 191
 Db 6056 GGCTCTAGCAGATGATCTTTTCATGGGGCCGAGCATGTGATAGACAGGTTCCGAGACT 6115
 QY 191 ----- 191
 Db 6116 TGATCTGGAAGCCCTTTTCTGCTGAAGGAATGGATCTTGTCACTCAGTGGTGTGTAT 6175
 QY 192 -----Thr----- 192
 Db 6176 GCTCAAGTCAATGTCAAAACTTTTCTGTTGGATCAGAGACTATCCAGGTACCTGTT 6235
 QY 193 -----Arg-----GluGlnSerGly----- 197
 Db 6236 TGAGATCCGGGACTGGCGGCTAATGGGTGCACTTGGGGCACTGAGCAGAGTGGCCAGCC 6295
 QY 197 ----- 197
 Db 6296 ATGCTCCCGCTGCAGCTCAGATCCTGCATCTGGGGCTTCCCTGGGGTAAACGTGGCAGTAGA 6355
 QY 198 -----Asp-----Tyr-- 199
 Db 6356 AAGAAACATGCCCCCACTCAAGTTTTTACATGACTTCCACTCGGAAATGTTCCAGTACAC 6415
 QY 200 -----GluCys----- 201
 Db 6416 AGTGTGTGGGGCCCATGTTGGATCCAGCTGGACACTGATTTGTTGCTGAGTGTGGACT 6475
 QY 202 -----SerAla-----Ser----- 204
 Db 6476 CTTGACTAAGCCTTCAGCTGAGCCCCAGCCCACTTTTGCCCTGGTGGGATAGAGCCGCT 6535
 QY 204 ----- 204


```
QY 280 -----LeuLeu-----Phe-----Asn----- 284
Db 8756 ARACTGAACATCTCATCAGATGTTTAAAGATTTCACCTGCAGCGACCAATAAAT 8815
QY 285 -----ValSer----- 286
Db 8816 GGAGCTTCGAAACAACAGGAAGATGTGAGTGGTCCGTCGCACCGAGTTTACTTTGC 8875
QY 286 ----- 286
Db 8876 TCAGGCAGTTGGCGCTGACAGAAGAAGATGGACAGCTGGGCAATCAGCTGGAGCT 8935
QY 287 -----As----- 289
Db 8936 ACAGAGTTCCTTACAGCAAGGTGAATAATCTGATGACACAGACATCTCCCTGGA 8995
QY 289 pTyGly-----Asn-----Tyr----- 293
Db 8996 GTTGGGCTGGTCACTATGAACAACCTTCTCCCTAATGCTATTATTAAGGTGGTCTTAAG 9055
QY 294 -----ThrCys-----ValAla-----SerAsnLys-- 300
Db 9056 GCCCAGAGTTCCTGCCAGTCTGGACACAGCTAGCCCTCGCCTCTTCCAGC---AAAGT 9112
QY 301 -----LeuGly-----His-----ThrAsnAla----- 306
Db 9113 CCAGCCACCTGTTGGTGGTATCTCTGTTAAGGAACACTTTGAGGTAATGTGGCTCT 9172
QY 307 -SerIle-----Met-----LeuPhe----- 311
Db 9173 CACCATCCAGCTGCCACCGCTTCTCCATAGAAATGATGGCTTTTCTTCTCTGGTCG 9232
QY 312 -----Gly-----Glu----- 318
Db 9233 AAATGTAGAGATGATGAAGTTGGTGTGATGAAGAGGATAAGTCCAACTGTGTACTGG 9292
QY 312 Y-----Pro----- 313
Db 9293 AATACCAGTTGTAAGCTCGCAGCTGTAGCAACAGATGATGATGATGATGATGATGATG 9352
QY 314 -----Gly---Ala-----Val-----Ser----- 317
Db 9353 CGGGAAGGGCGTGGCACAGGGCTTGACAGAGTCTCGAGTCAGAGATCATTTGCCAA 9412
QY 318 -----Glu----- 318
Db 9413 ATTACCTGAGCACCAGTTGATGATATTTGACAGATGAAGAGCGAGCTCCCATGAACA 9472
QY 319 -----ValSer----- 320
Db 9473 CTCCTTCATATATAAAATCCCAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 9532
QY 321 -Asn-----Gly----- 322
Db 9533 GAACAGTGGACTGGGGCGACCTTAACCTGGTGTACCTGCTGCTGCTGCTGCTGCTGCTG 9592
QY 323 -----Thr-----SerArg----- 325
Db 9593 CAGCTGACATGGCTGGACTTTGCCATGGCTGTCAAAAGGACGACGCGAAGAGCTCTGGT 9652
QY 326 -----Arg-----Ala----- 328
Db 9653 TGCCAGGTAAACAAGAAAATAAGGCTGAAACCTGCAACCGGGTCTGAGGTCCGGGG 9712
QY 328 Y-----Cys----- 329
Db 9713 AAAGTAGAACAAGGTGACCTGAACATGCAACAGCAGGAGAGAGAGAGAGAGAGAGAG 9772
QY 330 -----Val----- 330
Db 9773 CCTCAITGGTTAAGTGTGGCGCAAGAACCTTGGCAGAGCTTCCATCTTCCGCGAGCG 9832
```

```
QY 330 ----- 330
Db 9833 CAAGTGATGGAGACCAAGTGAAGTACTACATATAGATTGACTCTGGCTCAGGATCCAGG 9892
QY 331 -----Tip-----LeuLeuPro----- 336
Db 9893 GACTTGAGGGTGGGAGAGCTTCCCTTCATCTGCAGGATTTGTGGGCGCATATGGGAACT 9952
QY 336 u-----Val-----Leu----- 338
Db 9953 GAGAGACATTTTCAACAGCTGGCTCTGCTGCGAGGCGCATGTGGACAAAGCGCTGGGT 10012
QY 339 -----His----- 339
Db 10013 TCCTCTCATGGATTTAGACCCAGGCGCCACAGGGGCAAGAAACAGAGACCCAGGGAT 10072
QY 340 -----LeuLeu----- 342
Db 10073 TGTGTCCAGCCTAGTATCTCTGCTCTTTCGGGCAACAGAAAGGTTGGGGGATAGTTT 10132
QY 342 u-----LysPhe 344
Db 10133 GATCAAGTATGATAAATTT 10151

RESULT 23
AY405009 9744 bp DNA linear GSS 12-DEC-2003
LOCUS Homo sapiens HCM2081 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY405009
VERSION AY405009.1 GI:39760983
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 9744)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TODD, M.A., TANENBAUM, D.M., CIVELLO, D.R., LU, F., MURPHY, B.,
FERRIERA, S., WANG, G., ZHENG, X.H., WHITE, T.J., SHINSKY, J.J.,
ADAMS, M.D. and CARGILL, M.
Inferred nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..9744
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>9744
/locus_tag="HCM2081"

Alignment Scores:
Pred. No.: 8,73e-13 Length: 9744
Score: 1672.90 Matches: 270
Percent Similarity: 11.31% Conservative: 64
Best Local Similarity: 9.14% Mismatches: 9
Query Match: 69.47% Indels: 2611
DB: 29 Gaps: 263

US-10-017-084A-523 (1-344) x AY405009 (1-9744)
```

QY 1 Met-----Lys---Thrile-----4
Db 828 ATGGATCTTTGGAATCAACCATCGGATTCATCAACAATGGCTCTCCTGATGAAGGTGA 887
QY 5-----Gln-----5
Db 888 TATTTCCAGGGGCAITGCTGATCAAGAATAATCATTTGCTGGTGGTGGTGAATAATACCAC 947
QY 6-----Pro-----6
Db 948 ATGGATGTTTGAACCCCAACCATCGACACACTTGGGGCTTATTCTTCTGACACTGTAGA 1007
QY 7 Lys-----MetHis-----9
Db 1008 AAATCGAGAGAAATTCCTGAGCTAGCCAGAGGAGATGCTGCACAGCTCGGTGGATGTT 1067
QY 10-----Asn-----Ser-----IleSer---13
Db 1068 TGAACAAGGCCAATTTGGACTCAATGAATAAATGTCATCAAAAGTCAAGAAGATCAGCGGT 1127
QY 14-----Trp-----AlaIle-----16
Db 1128 AACTATCAGTAGGACATACCTGGGGGGATGCTCAAGACTGTGAGATACATGTTTGAAC 1187
QY 17-----PheThrGly-----Leu---AlaAla 22
Db 1188 TCAACATCTAGATCAACTTGGACAGCTTCATTCACTGGATGAGGTTCATTACTCAGCT 1247
QY 22-----22
Db 1248 TAGGCTGAGCTCAAGAAATTAAGGAAATGTTAAAGAGATGATAAATGTTTGAAC 1307
QY 23-----LeuCysLeu-----Phe-----26
Db 1308 TCAACATATATGTTATAGTAGGTTCGGGCCAAATGCTGGAAATTAATACTGTTC 1367
QY 27 Gln-----Gly-----28
Db 1368 CAGAGAAGCGTTGAAAGGGGAGATGTAAGAACAGCAGCGGTGGATGTTTGAACACACAGCC 1427
QY 29 Val-----Pro-----Val-----31
Db 1428 GTTGACACAAATTAACAAGATATACAGAAATTAAGTGTGCCGGAATATCATGGA 1487
QY 32 ArgSer-----GlyAsp-----Ala-----ThrPhe---38
Db 1488 AGAAATGTCAAAGGTGGGTGAGTAAGCAAGGTGTTATTGTAACCCCACTTTGGA 1547
QY 38-----38
Db 1548 GAAATCAAGAGTCAGAGGTCATCATTTGAAAGGAAATAATATAGGTACAGATGT 1607
QY 39-----ProLysAla-----Met-----42
Db 1608 CTCAGAAAGTGTGGATGTTGAAACCCA---GCCATTAGACATTCATAAAGAGGTTC 1664
QY 43-----AspAsn-----44
Db 1665 TGATCAGATTCCTACACAGGTGAGGAGATATAGTGTGGTGGTATACAACTACTAAGCA 1724
QY 45---Val-----Thr-----Val---ArgGln-----49
Db 1725 TCTATTGAAACACTTCCAAITGAAGCATTAAGACAGAGTCTTGATATAGGAAAGCTTCA 1784
QY 49-----49
Db 1785 AAAATCACTGCCTCTGAAGAGAAAAGCGGATGTTAGGCATCAAAAATGGATTTTGA 1844
QY 50-----Gly-----Glu---51
Db 1845 AACCCAACTCTGGAAGACATTAGAAAAGATATAAAGGAGGTACACACGACAGTGAAC 1904

QY 52---Ser---Ala-----Thr---Leu-----55
Db 1905 TGAAGAATTTTCAACAGAGAGATGTGAAGAATTACACATATCTTTGATCAACAATTT 1964
QY 56-----ArgCys-----57
Db 1965 AATTAAATTTGATGATCATCATAAAATAGAGGTGAAGAGTTTACAAGAGGTGCTGTAGA 2024
QY 58 Thr-----Ile-----AspAsn-----Arg-----62
Db 2025 GTTAAATAAATCTCTCTTCGAGACACACCACTGTATGCCATTCACAGATCCCTTTGAAA 2084
QY 63 ValThr-----Arg-----65
Db 2085 ATATCATCAAGTAAGACAGCTCCAGCAAGAAGAAATCGTAAGAGGTGATGAAGAAGCTG 2144
QY 66---ValAla-----67
Db 2145 TAGGTGGCTTTTGAACAAGGCCCAATTGACCAAGTTTGTGATCAAAAGCATTCATAAATTTCA 2204
QY 68-----Trp-----68
Db 2205 AATAATTAGAGGATATCTGCTCAAGAAATACAGACTGGAAATGTGAATCTGCCAAATG 2264
QY 69-----LeuAsn-----70
Db 2265 GTTGTGTTGAAACCAACCTCTTGTATCAATTAATATTTTGTAGTGTGGAAGAAACAGA 2324
QY 71-----Arg-----71
Db 2325 AAGTAAACTGAACAACTAGAGATATGTTAAAGGGGATGTCAAAACCTGTAAATGGCT 2384
QY 72---Ser---Thr---Ile-----74
Db 2385 TTTTGACACCAGCCAATGGAGTCTCTTTATGAAAAAGTTTCGTTAATGACCACAGTGA 2444
QY 75-----LeuTyr-----76
Db 2445 AGAAATTCATAAGGGAGATGTCAAAACCTTGTACTTGTGCTCTTTGAAACTCAGCCACTGA 2504
QY 77-----Ala-----GlyAsn 79
Db 2505 TACCATAAAGATGACTCTGAAACAGCAGTCAAAATTCGAACTGTAACACAGGAGAGAT 2564
QY 80-----Lys-----81
Db 2565 CCAAGGTGGGATGTTGCTACAGCATGTTTCTTTTGGACACAGAAATTTGGACAGCAT 2624
QY 82---Trp-----82
Db 2625 ACAAGGAGAGAGACTGAAGGAAATCAAGCCTGTTGAAATGGATATACAAGCTGGAGATGT 2684
QY 82-----82
Db 2685 TTCCAGCATGGGTATAAATTTGAAATCAGTCCTTAGATTCATATAAGTTCTAGTTTCA 2744
QY 83-----Cys-----83
Db 2745 GGAAGTTTGAAGAAGATCAAAACCTTAAAACTGAAGATATTCAGAAAGCAATGTTT 2804
QY 84---Leu-----Asp-----ProArg---87
Db 2805 AAATTGTAGTGGCTTTTGAACCAACCACTTAAGATAAAGAAAGAAAGCAAGG 2864
QY 88-----Val---88
Db 2865 TGATGAATGTTTAAGACGGTGCACAGACATACAGGTGGGATGTGAAGAAGGGTGTCT 2924
QY 89---Val---LeuLeu-----91
Db 2925 TATTTTGAGACTTTTCTTTTAGATGAGATTAAAGAGAAATCTGACTATATCAGACCAA 2984
QY 92---SerAsnThr-----Gln-----95

Db 2985 GAAAACAAATTACTGAAGAGATATACAGGGTGATGTAAAGAGCTACAGAAATGCTCTTTGA 3044
QY 96 -----Thr-----
Db 3045 AACCCAGCCACTCTATGCAATTCAAGACCGAGAGAGGTCCTATCATGAAGTGACACACAT 3104
QY 97 -----Gln-----
Db 3105 TAAAGAGAGAGGTAATTATGAGAGATGTGCGAGGAACAAGGTGCTTTTGAACAAA 3164
QY 98 -----Tyr-----Ser-----Ile-----
Db 3165 GCCATTAGACTCTATTAAATCAAGAACTGTGTATGTATTAAATCTGTGCACACA 3224
QY 101 -----Glu-----IleGln-----Asn-----Val-----
Db 3225 AGACATTCAAGAGGAGAGTGTAGTTCTGTGCAGATACAGATTTGAAAACTCAGCCACTGGA 3284
QY 106 ---Asp---Val-----Tyr-----
Db 3285 TCAGATTCTGAAGAAATCAATAATATTATGCCAGTATTTGACCATATACAAGGTGGCAA 3344
QY 109 ---Asp---
Db 3345 TGTAAAGACAGTAGACAAATCTTTGAGTCTGAAATTTTGTAGAAATAACTATATATACG 3404
QY 111 -----Gly-----
Db 3405 AACAGTAAGTGTCAATGAAATACAAAAGGGCAATGTAAACATCTACTTGGCTATTGA 3464
QY 112 ---Pro---Tyr-----Thr-----
Db 3465 AACCCACATATGGATGAATCTGAGAGAGAGAGGTTAGAAATATGAANAATATCAAGACGT 3524
QY 115 -----CysSer-----Val-----
Db 3525 CACTCAGGAAGATGTGCAGAAAGGTGATGTAAAGCAGGCTGTGTGCTTTTGAARAATCG 3584
QY 117 -----
Db 3585 AACTTTGATCTTATTTATGAAGCACATAAAGGTATCACAAAATGACCAAGAGAAAT 3644
QY 118 -----Gln-----Thr-----
Db 3645 CCTCCTTCTGATGTCAAAACACACATGGCTCTTTGAAACACACCCTTCATGAAT 3704
QY 120 -----Asp-----
Db 3705 TAATGAACTAGAGTAGAAGATAGAAATTTATGGCAAGAGCATTAAGAAACCTTAGA 3764
QY 121 -----AsnHis-----
Db 3765 AGATCTCTACTCTCAAAAAGTTATCAGGCTCTCTGGAATCATCATTTGAAGCTGATGAAT 3824
QY 123 -----Pro-----
Db 3825 AGGGATGTTGCAATGGCAAAATACAGCTAATGAACCAAGCATCTCTCGAGATACAGAA 3884
QY 124 -----Lys-----Thr-----
Db 3885 AGAAGAAATATCAGGCTGATCTCAGAAATATAATAGTGTGAACCTACTTTCCAAAAGGGA 3944
QY 125 -----
Db 3945 CTGTACTGAAGAGAGATTTTGATTAGTGAAGAAGAGAGGAAATGTTAATTTGACTAA 4004
QY 126 -----Ser---Arg-----
Db 4005 AACTCAATTATTAACAGATCAACTGAATTTTCATGCTGAAAAGAGAGATAGTGAAGG 4064
QY 128 -----Val-----His-----
|||

Db 4065 TGATGTACAAACAGCAATATAAAACCTGTTCTCTGAGGAAGATCTGTAAAGAAAGGCAT 4124
QY 130 Leu-----
|||
Db 4125 CTTAATTTCAGGAAGATGAAAAGGAGATATTAAACATGACTATCTATTGTTCTTCATGA 4184
QY 130 -----
Db 4185 AAATGATGGTGACACAAATTGAGCGTGAAGAAGTAATAGGTGGTGATGTCAAAACGTACCAT 4244
QY 131 -----IleVal-----Gln-----
|||
Db 4245 TCATAATTTATTGTTCTTCACATCAAAACATAAATAATCTGAAAGGGCTAAATAATGATGC 4304
QY 134 -----Val-----
|||
Db 4305 CTCTGAGAGAGAAATGTTCAAGTTTTCACAACCTGCATAGAAGCTGGAGCTTTGGATTGA 4364
QY 135 Ser-----Pro-----
|||
Db 4365 TCTGAAACAACTCCACACAGAGTCAATGAAACACTGACAGCTAAAGAAACAAAGAGGAGA 4424
QY 137 -----Lys-----Ile-----Val-----
|||
Db 4425 GAAAGAAATCATTTGGTGGTGATGTTGAAGGTACAAAACCTGTTACTGAAGAAAAGGCAGTC 4484
QY 139 -----
Db 4485 TCTGGTTGAACGTACTGTTAGTGAACCTGACATCATCCCTGGAGATGTGCATAACACAGT 4544
QY 140 -----Glu-----
|||
Db 4545 TAAAGTTTTTATGACGAGCCTCAGAGTACATTTGGTAAGATACCCAAAGAAAGAGATTAT 4604
QY 141 -----Ile-----Ser-----
|||
Db 4605 AAAAGTGATTGACATCAACCTAAATTCCTCAGCCAGGCTGTAAATCAGAAAACAGT 4664
QY 144 Asp-----
|||
Db 4665 GACGAAAACAGAAAGAAATTAATAAGGTAAACATGCTAGCCACACTCAAGTCACCTAAAGA 4724
QY 145 Ile-----Ser-----Ile-----
|||
Db 4725 ATCAAGCCATCGATGGAAGAAGATCTAAACAGCCTGATGCCATCCCTGGTGATTTGAAA 4784
QY 148 -----Asn---Glu-----
|||
Db 4785 AGCTATTGAATGCCCTTGAAGAAAGCTACAAATACAAAGACAGAAATTCGAAAAGAGGAGCT 4844
QY 150 -----GlyAsn-----
|||
Db 4845 TCTCAAGATGACCTGGAACATCATCTAAGGTCTTTGAAAGAAAGCACAAAGAGTTTCAA 4904
QY 152 -----Asn-----Ile-----
|||
Db 4905 AGAGTACATAMAGAAGGTGTATATAAAAAGNCTAAAGCTGTGTGATGGCAGGATCCTC 4964
QY 154 -----Ser-----LeuThr-----Cys-----
|||
Db 4965 GGGAGAGCAGAAAACAGATATTTCATCAGTTGCTGTCTCCAGAGGAACAAAATAGTCTTCT 5024
QY 158 -----Ile---AlaThrGly-----
|||
Db 5025 TCAGCCAAAGCCAGGTCCATTGTAGCCAGCGCCCAAGTGGCAAGGGGAGCAGACTACTCT 5084
QY 162 -----Arg-----
|||
Db 5085 CAGTCAAACTATCGGGAAATCTTGCCATGGCNAATTTAGTAGAAGAAAGACTGAGGTTAA 5144
QY 163 -----Pro-----
|||
Db 5145 TCTTCCAAAAGCCCCCAAGGCACTGTAAAGATTGTTCATAGATTGTGTAAACAAACATGA 5204

QY 164 -----Glu-----Pro-----ThrVal----- 167
Db 5205 TGCTCTGGAGAAAGCCTTTAGAGACTATCTAATTACACCATAAATCTAATGTTTGGG 5264
QY 167 ----- 167
Db 5265 ATCAGGAGACAAAACGGGTGCTGGACTGATCTACAGAGACAGCATCTTAGAGATGA 5324
QY 168 -----Thr----- 168
Db 5325 ATATATGAGCAGACAAATTAACCTCACTGTGTCTAAGTAATCTAACAACTTAAGA 5384
QY 168 ----- 168
Db 5385 ATCAGACAGGCGAGTGAGAGAGCTGAAGAGGATGATCTTTAATTCATCCCAATGCG 5444
QY 169 Trp-----Arg----- 170
Db 5445 TGGTAAACCGTTGGAGAGCAACACACATATCAACTGAGAAATGACCACAGAAAATGGA 5504
QY 170 ----- 170
Db 5505 GGGTTTTCATATAAGAGTCTTAAAGAGCAAAAATATTAAATATTAACTGATACACA 5564
QY 171 -----HisIleSer----- 173
Db 5565 AAGCTCCAGCCAGTCCGCCAGCATCCAGTCAGCATGCCAGTTGGAGGAATTCAGGA 5624
QY 174 Pro-----LysAla-----Val----- 177
Db 5625 CTTTCAGGGACTTTCAGAGCAAACTTTGTGTAAGCAAGAAACAAATATTCTTAATA 5684
QY 178 Gly-----Phe----- 179
Db 5685 GGATATAAGAAAAAGAAATATAAACCTTCAACCAATGTGGCAGCTTTTGGCTGTAGACA 5744
QY 180 -----Val-----SerGlu----- 182
Db 5745 AGACACATCCCATGTAAACAGAAATGAAAGTCTCTGAAAAAGTCAATATCAATTAAGGC 5804
QY 183 -----Asp-----Glu----- 184
Db 5805 AACCACAAAAAGCGGGAGACTGATGTTCACTTGAAGAACCCAGGACTTTCTAATGAAAAC 5864
QY 185 ---Tyr-----LeuGlu----- 187
Db 5865 AAATACTTCCACAGGCTTAAATGGAATGGCAATGGAAGAGTCCCTTGAATCCAATCAACTTAA 5924
QY 187 ----- 187
Db 5925 CCTGAGAATAATGTAAAGAAAGTGAAGTGGCCCTTCCACCTCCATCTCCACCTCCTCC 5984
QY 187 ----- 187
Db 5985 ACCACCTTCTAATGCATCATCTGAAATGAATTCCTCTCTCTCTCTCTCTCTCTCTCTCT 6044
QY 187 ----- 187
Db 6045 GATGTTTCTGAAAAAATGGGTTTCTTCCCTCACTGTCCACAGAGAAGATAAGGCTGA 6104
QY 187 ----- 187
Db 6105 ATTTGAAGTTTTCAGGCTCCCTCTTCTCCACCTCCAGTAGATGAGAAATCTGAAG 6164
QY 188 -----Ile----- 188
Db 6165 AGAAAGTTCAUCGATGTTTCTGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6224
QY 189 -----Gln----- 189
Db 6225 ACATCTCCTTCTCTCTCTGCTCCGGAAGAACAGCAGTGGAGACTTTCATGCAACAATATTC 6284

QY 190 -----Gly----- 190
Db 6285 CCAAAAAGAGCCTCGAACTCTCAGAAATTCCTCAGGCTAAAAATCATACAGGAAAAACCGG 6344
QY 191 -----Ile-----Thr-----Arg----- 193
Db 6345 TGTGTTGGCAGCTCCACATTCGCCAAACCCCAACTTCCCAAGCATATATAAGATATAATA 6404
QY 194 Glu-----GlnSer----- 196
Db 6405 GAAAGATTTTCCCCCAAGTTGAACCTGGCAACCTCCTCTGTGAGATATGGAATGTAAAT 6464
QY 197 ----- 197
Db 6465 TACTACCTCAAGGATCAGAAAAAGTAATGGTGTGATGACCAGCAGTGAACACACAGAGAC 6524
QY 199 ---Tyr-----Glu-----Cys 201
Db 6525 AAAGCAGAACCTTATTAGTAAGAGCTTTGATGAAGAAACAAATATTATCTATTGACTCTGC 6584
QY 202 -----Ser-----Ala 203
Db 6585 AAAGTGTCTCTCACACACAGTTCAGGAACCTCAGCAACCAGGAAAAAACAGATTGGCC 6644
QY 204 Ser----- 204
Db 6645 TCATTATAAATCTCATTCATTTCCAGAGAGTTCCAGGACAACAANAATCCAAAACCTTATAT 6704
QY 205 ---Asp-----Val----- 207
Db 6705 GAGAAATTTAAGACACCTTTAATGATTTGCTGAAGAAAAATATAGACAACAAAAGAAGA 6764
QY 207 ----- 207
Db 6765 AATTGAAAAACAGAAACAGGAGAGTTCTTACTACAACATTTGTTAAACTCAAAGCCAAA 6824
QY 208 -----Ala----- 208
Db 6825 TCAACACATAACAGAGGTGGAAGGAATGCCATTACAAAAAACCAATGAGGAGGTTTC 6884
QY 209 ---AlaPro----- 210
Db 6885 CCTATCTGGAATGATTACAGAACTGCTGTGGTTTCAACCCAGCCAGGCTCTCAAAGTAA 6944
QY 211 -----Val-----Val----- 212
Db 6945 TGCTCGGATACTAGGAGTGTCTCTGATAACCAACTCTCCACAACATCGCCAGAAACAGT 7004
QY 213 ---ArgArg----- 214
Db 7005 CGCTGCCAGAGGGCTCCACCATGTTTTCAGCAGCTTCAGAGAGCAAAAGTAAGATGAATAA 7064
QY 215 ---ValLys-----ValThrVal-----Asn----- 220
Db 7065 GGAAGTTTTCAAAGCTCAAGGACATTTATGCAATCCAATCAGCTTTCGGAATTAACA 7124
QY 221 ---TyrPro----- 222
Db 7125 AAGTCACCAAGATGTAGTAGTACCCCAACAAACACACAGAGAAGATATTTGGAGCAGTTGCA 7184
QY 222 ----- 222
Db 7185 CTTGCCCAAGCAACCAATTTCCCAATTTCAAAGTTAAACCAATCAAACTTCCAC 7244
QY 223 ---Pro----- 223
Db 7245 TCTAGATACATACATTAATGAACAGACACAGCTATGAAAGTCATAAAGCAATCTGA 7304
QY 224 ---Tyr-----IleSerGlu-----AlaLys 229
Db 7305 GATTGATGTTCAAAACCTTTTACCAAAAAACAATATCTGAAAAACCAAGAAAACTGAAGCAAG 7364
QY 230 -----Gly-----Thr----- 232

QY 338 -----Leu-----HisLeu-----LeuLeu 342
 Db 9585 AACCCAGATGCTTCTGCAACTGAGATGAGAACCACTTCCAGAGGAATCTGCATTAT 9644
 QY 343 Lys -----Phe 344
 Db 9645 AAGTGAAGCTGCTCCAGACAGCAAGGAATATGTATATCTTT 9686

RESULT 24
 AK090135/c
 LOCUS
 DEFINITION
 SR-4987 cDNA, RIKEN full-length enriched library, clone:G431004D19
 product:fibronectin 1, full insert sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 9279253
 10349636

REFERENCE
 2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
 Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 11042159

REFERENCE
 3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
 Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,
 Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
 Yanamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
 Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,J.,
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861

REFERENCE
 4 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

REFERENCE
 5 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 8315)

REFERENCE
 7 Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
 Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,M.,
 Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
 Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
 Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
 Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
 Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
 Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
 Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
 Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
 Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
 Muramatsu,M. and Hayashizaki,Y.

TITLE
 JOURNAL
 Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail:genome-res@gscc.riken.go.jp,
 URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
 Fax:81-45-503-9216)

COMMENT
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL:http://genome.gsc.riken.go.jp/
 URL:http://fantom.gsc.riken.go.jp/.

FEATURES
 source
 1..8315
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="BDF1"
 /db_xref="FANTOM DB:G431004D19"
 /db_xref="MGI:2429041"
 /db_xref="taxon:10090"
 /clone="G431004D19"
 /sex="female"
 /cell_line="CRL-2028 SR-4987"
 /cell_type="stroma cell"
 /tissue_type="bone marrow"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="5 months"
 194..7626
 misc_feature
 /notes="fibronectin 1 (MGD|MGI:95566, GB|X93167, evidence:
 B2ASTN, 99%, match=4434)
 putative"
 8296..8301
 /notes="putative"
 8315
 /note="putative"

ORIGIN
 Alignment Scores:
 Pred. No.: 4.54e-13 Length: 8315
 Score: 1671.20 Matches: 276
 Percent Similarity: 13.23% Conservative: 55
 Best Local Similarity: 11.03% Mismatches: 12
 Query Match: 69.40% Indels: 2159
 DB: 11 Gaps: 239

US-10-017-084A-523 (1-344) x AK090135 (1-8315)

QY 1 MetLysThr--Ile-----Gln-----5
 Db 8298 ATTAAACACTTGTCTTCCACAGTAGTAAAGCGTTGGCATGTGCTTATAAAATAATCA 8239

QY 6 Pro-----LysMetHis-----Asn 10
 Db 8238 CCAACCAATATTAAGTAATCTCTTATCAACTGCATCAAAAGTGTCTTCAATACAT 8179

QY 11 -----SerIle-----Ser-----13
 Db 8178 TTTTTCGTATAAAATCTGGGAAAATTTGATAAATAACAACAGTAAGAGAAAGGTA 8119

QY 14 -----Trp-----AlaIlePhe-----17
 Db 8118 TTTCTAGCAATCTGAATTGTTGGGACAAAGTGAGTCTCTGTGGAGGGGTGTTTGAACAC 8059

QY 18 -----ThrGly-----LeuAla-----Ala-----22
 Db 8058 ACAGCCACAGGCCCATGTCCTCGACAGTCTGTCAGGTGAGTGGCAAAAGACGAGAGGTG 7999

QY 23 -----Leu-----Cys-----24

QY 122 -----His 122
Db GTCTGGAGAAAGGTGATTTCTTTCAATGGTCCTGTCTCTTTTCGGGTTCAACCCGAC 5722
QY 123 Pro-----Lys-----Thr-----Ser----- 126
Db CCGGTAGCCAGTGAAGTCAACACTGGGTGGTCTATCCACTGGGCACTAAAGCTGGTGGGTGT 5662
QY 127 -----Arg----- 127
Db CACCTGACTGAACCTCAGATTGGTGGCGCAGGAATGGCTGTGAGTGGATTCCAATCAG 5602
QY 128 -----ValHisLeuIleValGln-----Val-----Ser 135
Db GGGCTGGCTCTCCCATATCATCTGCAAGCAACCACTGACTGTGTACTCAGACCCCGG 5542
QY 136 ProLys-----IleVal-----Glu----- 140
Db CCTGAGGCCCTGCAGCTCTGCAGTGTCTCTTCCACATCAGGTGCAGGGAAGTCCCG 5482
QY 141 -----Ile----- 141
Db GATTCATCTCCTCAGGCTCGAGTAGGTCACTCTGTACCTGGAACTTGCCCTGTGGCT 5422
QY 142 -----SerSer-----AspIle-----Ser----- 146
Db TTCCAGCAAAATTTGATGGATCGACATCCACATCAGTGAATGCCAGTCTTTAGGGCG 5362
QY 147 Ile-----AsnGluGly----- 150
Db ATCAATGTGTGCTCACTGCAGTTTGAACACAGGGCTGGCTTCTCGTTCCGGTCTGAGC 5302
QY 151 ---Asn---Asn---Ile-----Ser---Leu---Thr-----Cys--- 157
Db ATAAACACTAACCGACTACTCCACAGTGGGTGCAAACTTCAATGGTCAATTTCTGTG 5242
QY 158 -----Ile----- 158
Db ATCTGGACTGGCAGTTTATGTTTTTGTAGTCTCTAGGCCATTTTGGAGTGGTGGTCA 5182
QY 159 -----Ala-----Thr----- 160
Db TCTGTAGCTGTGCACAGGAGAAGTTGAAGGAGCCACCTGACACTGATGCTGTGTCCTG 5122
QY 161 -----GlyArg----- 162
Db GACATCTGTCACTGCATCTGGGACGGCTGTGCAATTTCTGTTTAAATTGATGGAAC 5062
QY 163 -----Pro----- 163
Db TGGCTTGCTGCTTGTGACTGTCCCGACGGCCAGTGACAGCATACAGGTTGATGGTGA 5002
QY 164 -----Glu 164
Db GTCTGCTCTGTTTAAATGTTGATGGTGGCTGTGACTGTGCTCCGGGACAGTGA 4942
QY 164 ----- 164
Db CTCCTGGACAGGCTATTTCTCTCTCTCTCGTAGGTGATTTCTGTAATAGCCGACAGA 4882
QY 165 -----ProThr----- 166
Db GACGGCAGGGGTTCCCACTGATGACAGGCTGGTGGGGTGGAGGCAATGACCTCCAG 4822
QY 167 ValThr-----Tyr----- 169
Db ATCTCTCGGAATATCAGAAACTGTGTGCTTGTGGCCAAATCAGTGGGGCTCTCTCTCT 4762
QY 169 ----- 169
Db GCCATTACAGCAATGATCTGACACAGTACTCGGTGCGCGGATTAAGTTGGTGGAGGT 4702
QY 170 -----ArgHis---Ile-----Ser----- 173

Db 4701 GATGGAATTCGCGAGGCGGCACTCGATCCTGCTGGGTCTTCCGACAGATGCTCGGC 4642
QY 174 -----ProLysala----- 176
Db GTGATGCGCGATGATGTAGCCGGTGATGGGGCCCGAGAGAGCCACCCAGTGGACAGTGAA 4582
QY 177 ---ValGly-----PheVal 180
Db TGAGTTGGCGGTGATATCAGAAGAATCAAAACCAAGTTTGGGAATCGAGACCTGTGTTCTG 4522
QY 181 ---Ser---Glu---AspGluTyr---Leu----- 186
Db CCTTCCCGAGAGGAGTGTCTCATGTGTTGCTAGACACTGGAGACACTGACTAAGTA 4462
QY 187 -----GluIle-----GlnGlyIleThr---Arg----- 193
Db TTCTGTCCAGGAGGAGATTGTTAGGACCAAGCATTTGCTGAAGGTGAATGGATAG 4402
QY 194 -----Glu-----Gln--- 195
Db CTCTGCAACGTCTCTTTCATTTCTACGGGTGAGTAGCGCACCAAGAGGTTGGTCAGCTC 4342
QY 196 SerGly-----Asp-----Tyr-----Glu--- 200
Db GATGACGGAGGCGGGCCCAAGTGACCCCGCATCGTCTCTGGACCGGATATTTGGTGAATCG 4282
QY 201 ---Cys-----Ser 202
Db CAGATCCGTGGAGAGGAGGACAGCCGTTTCTGTGTCAGTGTAGTAGGGGCACTCTCTCC 4222
QY 203 Ala-----Ser---Asn---AspVal-----Ala---AlaPro----- 210
Db GCCATTAAAGAGTGATAACGCTGATGTATAGTCAATGCCAGGCTCCAGCCCTGTAAAC 4162
QY 211 ---ValVal----- 212
Db TGTGTAGTATCTTACTGAGGAGTCCACAAAATCTTCAAAAATAGGGATCCCTTCTCTCGC 4102
QY 213 Arg-----ArgVal----- 215
Db CGCAACTACTGTGATTCGGTACCCGATAATAGTGGGAAGAGTTTAGCGGGGTCCACCTCAG 4042
QY 216 ---Lys---Val----- 217
Db GCCGATGCTTGAATCAGTTATATCAACAAGCTTAGGTGAGTGGGCGACCTCTGG 3982
QY 218 ---Thr-----ValAsn----- 220
Db GACAACGATATCAGAGATAGGGGCACTTCTCTGTCATCTTTGACAGTGTAAACACTGAC 3922
QY 221 ---Tyr----- 221
Db GTTGTACTCCAGGCCAGATTCAAGTTCTCAAAAGTCAGGAACCTCTGATCAGCATGGAC 3862
QY 222 ---Pro-----ProTyr----- 224
Db CACTTCTCCAGAGAGTCCCTGCTGCTGCCGTTCTGGGGGTAGTAGTTATTTCTGTAGCC 3802
QY 225 ---IleSer-----Glu----- 227
Db AGTGATATCTGGGTAGTGTCTCTCTCCAGGAGACAGTAAGCACTCCAGTGTGAGGGTT 3742
QY 228 -Ala-----Lys----- 229
Db TGCCTCCAGATGCAAGTTGGTTCGGTGGAGACAGCGGTGTCTACTCTCTGTTGACAAATCGG 3682
QY 230 -----Gly----- 230
Db TGCATCTCTCTCCCATCTCCGAGGACTTTGGATGGTGAAGTGTATTCCACGCTTGA 3622
QY 231 ---Thr-----GlyValPro----- 234

Db 3621 GTCAAGCCAGACACAACATGCTCCAGAGTCTGAAGTCACTTCTCGGGGTGCTCACCT 3562
QY 235 -----Val-----Gly----- 236
Db 3561 CCTGGCTCGTGTACACCCAGTGAAGCCAACTCTGGAGCGGGGTCCAGGTGATC 3502
QY 237 -Gln-----Lys----- 238
Db 3501 ACAATTGTGTCTGTGTACCTCGGTGTTGAAGTGAATGAGCGCAGAGGCTGCAGG 3442
QY 239 -----GlyThrLeu-----Gln----- 242
Db 3441 GTAGTAAGACTCCGGTGGCTTTGGGACTCTGTGTGGTTCCTTTCCAGCCACCAAGGTC 3382
QY 243 -----Cys-----GluAla-----Ser-----Ala-----ValPr 249
Db 3381 ACGGTGTACTCAGACCCAGCTGCAGATTCTCAGGGGATACTTGGAGGCCAAGGGTCCC 3322
QY 249 O-----SerAla----- 251
Db 3321 ACATTGTACTGTGGCTGGCTCCTCGGGTCAGGCCCGCGGTCACTCGGTAGCCTGCT 3262
QY 252 -----Glu-----Phe-----Gln----- 254
Db 3261 ATACGGGCTCGAGGTGGAGTCCAGGTACAGAACTGTTCTGTCAAGTTTCATTGACAAAC 3202
QY 255 -----TrpTyr----- 256
Db 3201 TGGAGGTAGTGGAGGCTCGAGTTGGTGTCTGTGTGCGGTCAAGAGATTGCTTCC 3142
QY 257 -----LysAsp----- 259
Db 3141 CTGCCCTGTGCACAGCAAAAGACTTTGAAGAGGTACGTGACCCAGGGAGACCCAGTG 3082
QY 259 sp-----Lys----- 260
Db 3081 ATTTCAGAAAGGTATTCTGTGTGACGAGCGCTCTGCCCATGTTTCCCGGCGAGGCTG 3022
QY 261 -----Arg----- 261
Db 3021 ACAGGCGAGGACTCCACACGGTATCCAGACACACACTATCAGGAGGGTCCACATGATG 2962
QY 262 -----Leu-----Ile- 263
Db 2961 GTGACTTTTACATCAGTTCACAAACTGTAGGTTCGTGCGAGGGGAGCTTATCA 2902
QY 264 -----Glu----- 264
Db 2901 GATCTTGGGGTGCCAGTGTCTCTTGTGTGATGAACAGGCTGTGCTCTCCTGGTTCCTC 2842
QY 265 -----Gly-----Lys-----LysG 268
Db 2841 TCCACAGCATAGATAGTGTGTGTACTGAACCCGGCTGCAGGTCTGTGAGGGTGACG 2782
QY 268 LysVal-----LysValGlu----- 272
Db 2781 GAGTTGGCCGTTTCAGGGAGGTTGAGTCTGTGCTACTGCTTCTACTGAAGGTGAATAG 2722
QY 273 --Asn-----Arg-----Pro----- 275
Db 2721 ACATTTCTATACCTGTGTAGTGTGCTGGGGTCTACTCCACCGAACACAATGGAAGTA 2662
QY 275 ----- 275
Db 2661 TCATCAACCTGGTCCAGGTAGGTCTGTGAGGAGCGTCAGGTCTGTAGTCTGTAGGTA 2602
QY 276 -----Phe-----Leus 278
Db 2601 GACAGGATCAAGTCTGTGTTTCCCTCTCTCAGATATCTGATPAGACATTGACAATGTACTTT 2542
QY 278 ex-----Lys----- 279
Db 2541 CTGCCCGGAGGAGGTGAGAAATGTTTCAAGAAAGTGGCCGCTGTGGAGATCAAGGTAC 2482

QY 280 -----LeuLeu----- 281
Db 2481 TGTGTTTCATCTCCCTCTCGCTCAGTCTATATCCACCGGAAGCCTGACACGGTGTG 2422
QY 282 -----Phe-----Phe----- 283
Db 2421 GAGGCTGACCCCATGACACCAAGCTGTGGCTGTGATTTTCAGTTTACAGATTTCAGAA 2362
QY 284 -----Asn-----Val-----Ser----- 286
Db 2361 GTGGCCACAACAGGAGGTAGGGCGCAGTCTCTCCGGTCACCGTGTGCTGTGTCACAGG 2302
QY 287 -----Glu-----His----- 288
Db 2301 GTGCTGGCCTGGTGTGAAGTTCGAAGCTGTCACTTCTGTGGCCATCTGCTGGATG 2242
QY 289 -----Asp-----TyrGly----- 291
Db 2241 CTGATGAGCTGTCCCTCATAGATCACACCTGGGTTCAGGCCTTTGATGTTATAGGATTA 2182
QY 291 ----- 291
Db 2181 AGGTGCCAGGAATGTAGTCTTCTTCCAGCGACCGTAGAGGTTTGTAGTCTCCATCTG 2122
QY 291 ----- 291
Db 2121 AGAATGTACTTGGTGTGTGAAGGCTCCGGGGCATTCCTGATGGGTGGGAATTG 2062
QY 292 -----AsnTyr-----ThrCys----- 295
Db 2061 GGTGCTGGGGTCTCCGTGATAATTACTTGGACAGGTCAGTGTGCTGTGGTAGGTC 2002
QY 296 -----ValAla-----Ser- 298
Db 2001 TGCAGAGTTGACAGTGCCACTCCCGATGCCAGCGCGGTAGCGTAACACTGGTATCG 1942
QY 299 -----Asn-----Lys----- 300
Db 1941 ACACCATGCACAACTTCTCCAGGAGTCACCAATCTGGTAAATGTCCGGGTCTCTGAA 1882
QY 301 -----Leu-----Gly- 302
Db 1881 TCTTGGCACTGTCAATGGGGTTCACACTTCCATCTGCCCGCCCTGTACCAAGACAGGTA 1822
QY 303 -----His-----Thr----- 304
Db 1821 CAGTTCCAGCATATGCTCCTCTCGTACGCTTGTGGAACGTGTGTTCAATTGTAAGTA 1762
QY 305 -----Asn-----Ala-----Ser- 307
Db 1761 ATGTCAATCAACATGCACACTGGTCTCGAGCTGGAGTAGGGATGCAGGCCCATCTCCA 1702
QY 308 -----IleMetLeu----- 310
Db 1701 CGACCGTTTCCCAACACACGTGCACCTCATCATGTGCGCCAGGTCTGCTTATCCCC 1642
QY 311 -----Phe----- 311
Db 1641 TGATCCCCAATCGGATACATGACCCCTTCATTTGTTGTGCAGATCTCTCTGTGGGCGAGC 1582
QY 312 -----Gly----- 312
Db 1581 ATTGGGCAATCCAACTTCTGTATCGGCATCGTAGTTCTGGGTGTGGCGCACCATTTTC 1522
QY 313 -----Pro-----Gly-----AlaVal-----S 317
Db 1521 ATGTTGTCTCCGACCCCTCAGAGTACAGTCCGGTGAATTCGGGTGTTGTGTACAGGAG 1462
QY 317 exGluVal-----Ser-----Asn----- 321
Db 1461 GGGAAAGTGACACAGAGCACCATTTGGAAATTCGCGCTCGAGTCCGAAACCAACCCCATG 1402

```
QY 322 --- Gly-----Thr----- 323
Db 1401 TCTGTGCAGAGGATACTTCGGTCTTGTGTAATGGAAGTGTGTACACACAGA 1342
QY 324 --- Ser-----A 325
Db 1341 TGTCCGCTTTCGGCCCTTCGGTGTGAGGATAGAGGCTTACCGTTGTAGTGAAC 1282
QY 325 tq-Arg---AlaGly----- 328
Db 1281 GGGAGACACAGGGCTCCCGTTTGAATGCCACATAAGTCTGGGTACGGCTGTCTCC 1222
QY 328 --- 328
Db 1221 TGGCAGCTCAGCCATTGCCAGGACGNGCAGACATTGCTTGTTCCTTGGCACTTC 1162
QY 329 --- Cys----- 329
Db 1161 AGCCACTGCATTCCACAGAGTAGACACACCACTGTCGGTGACACAGTGGCGTAGGA 1102
QY 330 --- Val-----Trp----- 331
Db 1101 GCGGCTGGGGTGTAGTCTCGCGTTGTGAATAGCTGTTGCGACATCAGTGAAGAGCCA 1042
QY 332 --- Leu-----LeuProLeu 335
Db 1041 GATCCGGCTGAAGCACTTTGTAGAGATGTCGCTCACACTTCCACTCCCTCTGCCATTG 982
QY 335 --- 335
Db 981 CCTGTGCACACACTGAAGAGGTTTCTCGGTTGTCTTCTGCTCCACGTGTCCTCA 922
QY 336 --- Leu-----Val-----LeuHisLeuLeuLeuLys----- 343
Db 921 ATCTATAGATGTCGGGTGTCCTGATCGTGTGATCTGTTCTCGAGGTACAGTGTATG 862
QY 344 --- Phe 344
Db 861 CGTCCATTGCTTCGCTAGACAGTACAGTCCACCATCATCCAGCCTTGGTAGGGCTTT 802

RESULT 25
LOCUS A0839851/C
DEFINITION 69115-c79 CITB Homo sapiens genomic clone 69115, genomic survey
sequence.
ACCESSION A0839851
VERSION A0839851.1 GI:6652483
KEYWORDS GSS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 22715)
Carpten,J.D., Makalowska,I., Robbins,C.M., Scott,N., Sood,R.,
Connors,T.D., Bonner,T.I., Smith,J.R., Faruque,M.U., Stephan,D.A.,
Pinkett,H., Morgenbesser,S.D., Su,K., Graham,C., Gregory,S.G.,
Williams,H., McDonald,L., Baxevanis,A.D., Klingler,K.W. and
Landes,G.M.
A 6-Mb high-resolution physical and transcription map encompassing
the hereditary prostate cancer 1 (HPC1) region
JOURNAL Genomics 64 (1), 1-14 (2000)
MEDLINE 20175426
PUBMED 10708513
COMMENT Contact: Carpten JD
Cancer Genetics Branch
National Human Genome Research Institute/National Institutes of
Health
Bldg. 36, Room 3D04, 36 Convent Drive, Bethesda, MD
Tel: 301 435 5626
Fax: 301 435 5465
Email: jdc@nhgri.nih.gov
Class: shotgun.
Location/Qualifiers
```

source

```
1. 22715
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="69115"
/clone_lib="CITB"
```

ORIGIN

Alignment Scores:

```
Pred. No.: 4.78e-11 Length: 22715
Score: 1670.30 Matches: 285
Percent Similarity: 10.74% Conservative: 43
Best Local Similarity: 9.34% Mismatches: 8
Query Match: 69.36% Indels: 2717
DB: 28 Gaps: 248
```

US-10-017-084A-523 (1-344) x A0839851 (1-22715)

```
QY 1 Met----- 1
Db 14794 ATGGGGTGTCTCAAGAACTATTATTAGTAGGAGGCAATATAAACCGGCATAAATTCTA 14735
QY 2 ---LysThrile----- 4
Db 14734 AACAAACAATTATCAAAAAGAACTTTGAGTACTTCTCTATGTTAAAGCAAGATCAA 14675
QY 5 ---Gln-----Pro----- 6
Db 14674 GAAGAACAGTAGAAGAACATCTCTCTCCCTAATATTATCTACTTTGTGTTATTGCTAA 14615
QY 7 ---LysMet-----His----- 9
Db 14614 AGAAATTAGTTGGAAGAGCTGTCCTATGTACAGGCAAGAAATATTAGTAGTAGGTG 14555
QY 10 ---AsnSerIleSerTrp----- 14
Db 14554 TAATTGAGTGTGATTGACTGATTAAACGGAATAAATATTGTTGTTCTTAAGAATAGGAC 14495
QY 15 ---Ala-----Ile-----PheThr 18
Db 14494 TGAGTATTGGAAGACTGTGGCCACAAGGTTAATCTCTTCTGGAAGCAACTGCGTATTACT 14435
QY 19 Gly----- 19
Db 14434 GGATTCAATTAAACATTTATATGACAGTATTACTCATTTTAACCTGTTACCACTT 14375
QY 19 --- 19
Db 14374 GGGAGAGAGCATTTCTCCAAGAAATTTGAAAACAGAGACAAGTGTGATTGATGGGAAAA 14315
QY 19 --- 19
Db 14314 GAGCAGGAAACTTAAGGGAATAGACAGTGTGGGAAACATATATCTCTGCTTGGGAGACCC 14255
QY 20 ---LeuLala-----Leu---Cys----- 24
Db 14254 TGAACATTGCTGCTGAGGAGAAAGGATCTCAGATGAATGTTTGTAGTCATTGCTTACC 14195
QY 24 --- 24
Db 14194 TTAATTATTAGTACAGCATTTTAAACATAAATATGGAATATGGAATTAACATTTATGGAAAA 14135
QY 24 --- 24
Db 14134 AATGATGATGATGATGATGATTAACATTTGAAATATCCACTAGTGTGAGAAATATT 14075
QY 25 ---LeuPhe----- 26
Db 14074 TCGAAGTTCTTGACACTTATTTTATTATTATTATTATTATTATTATTATTATTATTACCT 14015
QY 26 --- 26
Db 14014 GCGAGGTAGTACTGAAGTATAGAGAGATAGATACAGAGATTTTGGCCAAAGATTATGCA 13955
```


QY 192 --- ThrArg --- 193
Db 9586 AATCGGTAGAACTAGATAGCAGTAGGCAATATATGCTCTTTAGAGTTGGACTATTTT 9527
QY 194 --- GluGln --- 195
Db 9526 CTTTCACTGAATGAAGAGCCATTAAAGAGCTTCTGAGCAGGTAAATGACAATCCAATTCG 9467
QY 195 --- 195
Db 9466 ATTTTGAAGAGACTCTGATTAACAATATAGGGGCCAAATTTGAGGTTGATGAAACTTG 9407
QY 196 --- Ser --- 196
Db 9406 CTTTCACTGTTTCACTGAGACCTGTGAAGACAGTCTTCTGACTCTCTGACTCCATTCACACC 9347
QY 197 --- Gly --- 197
Db 9346 TAGAATTTATCTTAATGTGGCTTCTGTGGGACTTGTCTTTTCTAGTTTTTTTTC 9287
QY 198 --- Asp --- TyrGlu 200
Db 9286 TATGTTTAAATATATATGTTGTTGTTCCATTAACCTCATCTCATCATGATTTTGGAGC 9227
QY 201 Cys --- Ser --- Ala 203
Db 9226 TGTGTAACATCATCACTGTTTCTTTTATGCTTTAGTGTATAGTATAGCAATTTTGTCTGCA 9167
QY 204 Ser --- 204
Db 9166 AGTAGATCAATGCAAAATGCTTAATACTAAACCCAGGAACCTAATGAATGAGAACTTAGCTG 9107
QY 205 --- Asn --- Asp --- 206
Db 9106 ATGAAGTCAAGAACCCAGGACTGGATGGGTTTGTGATTTCTTCTGAAAGTATCAATGCT 9047
QY 207 --- Val --- Ala --- 209
Db 9046 GTCACTGTATAGAGACACAGTGGTTAGAGCACACTTAGAGCTAAGGTCATGCTTAACCTC 8987
QY 209 --- 209
Db 8986 TGCAGAGGGAGCTTGAACTTCACTGAAGAAATAATTTCAACTAGATCTAGACGAAC 8927
QY 210 --- Pro --- ValVal 212
Db 8926 AAACCAAGAGAGAAATTCACAAGGAATTTGTAAGGGCACAATGCAATGAATGATC 8867
QY 213 Arg --- ArgVal --- 215
Db 8866 AGAGCATGATGAGAGGGCTAGCTGAAGTTTGGGTGAGTGGGGAAGTGATGAAGGAAT 8807
QY 216 --- Lys --- 216
Db 8806 CAGACTAAAGTAGACTAGGCAATGGATGTGAAGGGCTTGTGAAGCCATGTTATGTTAA 8747
QY 216 --- 216
Db 8746 ACATACTATATGTTAGCCATGTTATGTTTCCATATGTTTCCATATGTTAGTCATATTGGCC 8687
QY 217 --- Val --- Thr --- 218
Db 8686 ATCGTGTGTTGTTTCACTCAGTTTAGAGTAAGAGGAAATTAGCTCACACTAAAACACTGG 8627
QY 219 --- Val --- Asn --- 220
Db 8626 GGAAGACCGATCATTAATGAAGAGCTGCTTTGTGAAGCAACAGGCAAAATATATCAAGAGTT 8567
QY 221 --- Tyr --- 221
Db 8566 CAGACAATRACTTACATAATGAGTTTTTAGCACAGCAATACTGAAATCTTCCCTTAAATAT 8507

QY 222 --- Pro --- Tyr --- 224
Db 8506 TTCCCTTCCCACTAGTTATCCAAATTTAAATATFACCAATAGGTTTACTATCATATTA 8447
QY 225 --- SerGlu --- Ala --- Lys 229
Db 8446 GCAAAATCTCATCAAAAATAGAACAGTGCACAGCTTATATCTCTGATGAATAAAG 8387
QY 230 --- Gly --- ThrGly --- Val --- Pro --- 234
Db 8386 TACCATGGAACCATCTAAACTGGCCCTACTACTACCAATAAATGAATGCCGGAATC 8327
QY 235 --- Val --- GlyGln --- 237
Db 8326 ATCTTCTGTGAATATGGAATAACCAAGTGAATAAAATTTATTTGTCATCCAGGATTTTA 8267
QY 238 --- Lys --- Gly --- ThrLeuGln 242
Db 8266 TTTCAATTTTAAACAATCTAGTTGGTAGAAACCTCTTCTCTTATTTGGACTCAG --- CAG 8210
QY 243 Cys --- GluAla --- SerAla --- 247
Db 8209 TGCCTTATCTCTTCTCCACTAGAAACCTAGTCATGATTTTCTATTTCTGCAATTCOAAT 8150
QY 248 --- Val --- Pro --- 249
Db 8149 CAATTTGATGACTGAGTGGGCACATGGCTGAGCAGGAATCTAAAATACATCCAGAT 8090
QY 250 --- SerAlaGlu --- Phe --- Gln --- 254
Db 8089 TCATCAATGAATAAATGATTCAGTGGCTGTATTTGCCAGGAATCTGGAAGGGAGAG 8030
QY 255 Trp --- Tyr --- Lys --- Asp --- 258
Db 8029 TGCAACTTGGCGATATGTTTTTTCATCCAAAGCTGAGACTATTTGAAGACAACTATAAT 7970
QY 258 --- 258
Db 7969 AGCTTACCATCTGTCTGTGAAATGGTTCCCATATATAATGCGCTAATACAAAGCATATC 7910
QY 259 --- Asp --- 259
Db 7909 TTAATAAAGTTTTTTTGGAGTGAATTTAAGACATTTGTGTAGCCCTCTAGAGTCATTTT 7850
QY 260 --- LysArg --- 261
Db 7849 TTTCTTGGACATCTAGACAAATGCCCTACCTTAAATTTTAAATGTTCTTACATCTTCTTCC 7790
QY 262 --- Leu --- IleGlu --- 264
Db 7789 CTCTTTACTATTGGTGTATTTGAATTTCTAGTACAGGGTTCTCCATTTGTTCTGTTAAAT 7730
QY 265 --- Gly --- Lys --- 267
Db 7729 TCATCTGGTTAGAGTTAGCTTGTTCACATATATTTTAAATTTACTTTCCAAATATTT 7670
QY 268 --- Gly --- Val --- 269
Db 7669 TGAGGTTTTAAGAGTTCTTGAATATATAATGATGCGCAGTGGATGGATGCCAAACAAATCCT 7610
QY 270 LysVal --- Glu --- Asn --- 273
Db 7609 AAAGTAATATAAATGCAATTCAGAAATATAGAATCCACAAAGAGGTAATAAGCTCA 7550
QY 274 --- Arg --- Pro --- Phe --- LeuSer --- 278
Db 7549 CTCCAGGAGAGAAATCACCTGCTCTCTAAATCTTATTTGAATTTCTTACTTATCTTTAAT 7490
QY 278 --- 278
Db 7489 ACTCAGCTAAAGCTTAATTTCTCCATGAAAACCTTCCCATTAATTCGCCAGTTGTAATGAC 7430
QY 279 --- LysLeu --- Ile --- 281

Db 7429 TCAGTTTGAACCTCTTTGAAAGAAATCAAGTCTCATGTTATTTTGGTATCTATCTTAG 7370
|||
QY 282 -----Phe----- 283
|||
Db 7369 GTCAGGTTCTATAGAAAAAGACTGAGATAAAGGTTCTCATGTAATACGTTGAAGGAGTGT 7310
|||
QY 284 -----Asn----- 284
|||
Db 7309 GCGATGATGAACCTGATGAGAGTGAAGAAAGATAAAAGAGGGAGAAAACCTCAGTAAAG 7250
|||
QY 285 -----Val-----Ser-----GluHisAsp 289
|||
Db 7249 AATGGGTTAGTTAGTCTTATCTCAGCTGATCCAGGGGAAACTCTTGAGCAATGAA 7190
|||
QY 290 -----Tyr----- 290
|||
Db 7189 AAACATCACAGAAATTATCTTATTTATAATAACATACACATTACAGGCAATTCAGAGCTCT 7130
|||
QY 291 -----Asn-----Gly----- 292
|||
Db 7129 TGTAACCCCTCATCAGTAGTCTACTGTTGACGCTTTCCTCAGGAGGAAGGCAAAACCAA 7070
|||
QY 293 -----Tyr----- 293
|||
Db 7069 CCATATCTCATCAGCTGAGAACAAATCTCAGAATAAGAAATGCAGCTGTAGATTTAGCA 7010
|||
QY 293 ----- 293
|||
Db 7009 GCCAATFACTCACAGCAGCTTGGAGATGAGTGTCTGACAGGAAAGGGGATCTGGACAGA 6950
|||
QY 294 -----ThrCys----- 295
|||
Db 6949 ACRACAGCAGTACCTGCTACAGTTCTCTCCAGAATCAAGTGTGGCATCTGCATGTATA 6890
|||
QY 296 -----Val----- 296
|||
Db 6889 AGACACAATAGATGCTTACTGATCTGTAGTGTATTAGAGAAATCAACATAATGCAACTCT 6830
|||
QY 297 -----Ala-----Ser----- 298
|||
Db 6829 TCTATTGCGCACATTTTATATATGCTATTCCTGTTTCTTATGCTTCTATACAGCG 6770
|||
QY 299 -----Asn----- 299
|||
Db 6769 AAAGGTGGCGTTAAATTTGATTTTAAATTTGGTAGTACAGTAATAGAGAAATATAA 6710
|||
QY 300 Lys-----LeuGly-----His-----Thr----- 304
|||
Db 6709 AAATCACTAGGATGTCACAAAACCTCTAACCCCTTAACTATTGTTGTAAGAGCTATGATGATGGA 6650
|||
QY 305 -----AsnAlaSer 307
|||
Db 6649 GAATTTTACGTTGATTTATTTCTTTTATTTGTTTATTTAAATATAATAAAT---AGT 6593
|||
QY 308 -----Ile-----Met----- 309
|||
Db 6592 AGGAATTACATTTGATCAGCTGTAGAAAAAAGAGTTAAAGAGTATGATGATGAAATGGGA 6533
|||
QY 310 -----LeuPhe----- 311
|||
Db 6532 GGCACGTGATAAATCTTTTAAATTTGTTTACAGAGATCCTCAACTGAAATTTCTGTTGCT 6473
|||
QY 311 ----- 311
|||
Db 6472 AATTTTAAGTAATTTTAACAGTATGAACACTGTGGAGCTTACAGAAAAGTTGCAATG 6413
|||
QY 312 -----Gly----- 312
|||
Db 6412 TGATAGGAGAGATGTTTCTCTCTGAGCCATTTTAGGAATAAGTTACTAATCAATGAGTT 6353
|||
QY 313 -----Pro----- 313
|||

Db 6352 CCATCACCCCTGAATAGTTTAAATGTTGCTTACTACAGATAAGGATAAATCTGCTACTATC 6293
|||
QY 314 -----Gly-----AlaVal-----Ser 317
|||
Db 6292 CACAATATAAGCATCACATCAGGATATTAGCAATTAGCAATTACTATGACCAACTTCA 6233
|||
QY 318 Glu-----Val-----Ser 320
|||
Db 6232 GAGCGCAATTCATATTTCCACAGTTGTTCTGCTGGCATCTTTTATCTGTCAAGTGAACAGT 6173
|||
QY 321 -----AsnGlyThrSerArg-----Arg----- 326
|||
Db 6172 TGGTGAACATCAATGGA-----AGAATTCAGGTCAATCCCATGTTGCTTTCAGTTG 6119
|||
QY 327 -----AlaGly----- 328
|||
Db 6118 TCATGTTTCTTTAGTCTTCTTCAGTCTGGAACAGTCTCTGCTCTTCTTCTGACTTGCTAAT 6059
|||
QY 329 -----Cys 329
|||
Db 6058 CTTTACCATTGGAAGATGACAGATGGCTATACATTTCCTTGCATTTGCAATTTGAGTTGCT 5999
|||
QY 330 -----Val----- 330
|||
Db 5998 CTGTCACTCTTCTGATGATTAGATTTCAGGTGCTGCACTATGCGAGGATATCACAGAAGC 5939
|||
QY 331 -----Tyr----- 331
|||
Db 5938 AATGCTACATTTCTTTCGCAATTCACCAAGTGGGGAATTTGCGTTTGCCTCACTGTGA 5879
|||
QY 332 -----LeuPro----- 334
|||
Db 5878 GAACACAGTTTGTATGATTTAGTCTGCCAGGTTTCTCTACAAAGCTTACTCTTTTCC 5819
|||
QY 334 ----- 334
|||
Db 5818 CTTTGTAAATTAAGTATTTATCACGAGCAAGTATTTTGAGATTATGTAATATCTGTTCA 5759
|||
QY 335 LeuLeuVal-----Leu----- 338
|||
Db 5758 TTATTAATCTATCTATCTATTTATCATCAATGAGTCAATGTTTCTCTATATTTCAATG 5699
|||
QY 339 -----His-----LeuLeu-----LysPhe 344
|||
Db 5698 GATCAATATCTGTTGCCAATTTATTTATTTGAATGTTT 5660
|||
RESULT 26
AQ839854 14771 bp DNA linear GSS 31-MAR-2000
LOCUS 260L13-C54 CITB Homo sapiens genomic clone 260L13, genomic survey
DEFINITION sequence.
ACCESSION AQ839854
VERSION AQ839854.1 GI:6652486
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Carpten, J.D., Makalowska, I., Robbins, C.M., Scott, N., Sood, R.,
Connors, T.D., Bonner, T.I., Smith, J.R., Faruque, M.U., Stephan, D.A.,
Pinkett, H., Morgenbesser, S.D., Su, K., Graham, C., Gregory, S.G.,
Williams, H., McDonald, L., Baxevanis, A.D., Klingler, K.W. and
Landes, G.M.
TITLE A 6-Mb high-resolution physical and transcription map encompassing
the hereditary prostate cancer 1 (HPC1) region
JOURNAL Genomics 64 (1), 1-14 (2000)
MEDLINE 20175426
PUBMED 10708513
COMMENT Contact: Carpten JD
Cancer Genetics Branch
National Human Genome Research Institute/National Institutes of
Health

Bldg. 36, Room 3D04, 36 Convent Drive, Bethesda, MD
Tel: 301 435 5626
Fax: 301 435 5465
Email: jdc@hgrl.nih.gov
Class: shotgun.

FEATURES

```
Location/Qualifiers
1. .14771
   /organism="Homo sapiens"
   /mol_type="genomic DNA"
   /db_xref="taxon:9606"
   /clone="260L13"
   /clone_lib="CTB"
```

ORIGIN

Alignment Scores:	
Pred. No.: 7.36e-12	Length: 14771
Score: 1667.90	Matches: 301
Percent Similarity: 9.35%	Conservative: 35
Best Local Similarity: 8.38%	Mismatches: 6
Query Match: 69.26%	Indels: 3252
DB: 28	Gaps: 255

US-10-017-084A-523 (1-344) x AQ839854 (1-14771)

QY	1	Met	-----Lys---Thr	3
Db	3621	ATGTCAGTACAGTGACAAGCTTTTCAGTAAAGAACACTTGTGTCTTTTAGAAGCTTACA		3680
QY	4	Ile	-----	4
Db	3681	GAATTAGCGTCGTCTTACAGCTGTAGTTTTAGATTGAACCTCGGAAAGTGGTTTTAT		3740
QY	5		-----Gln-----	5
Db	3741	GAGGTGTTACCGCAGGAGTGTATGATGCGAGTTGGATTGCTTACTCACAATTATTAT		3800
QY	6	Pro	-----Lys-----MetHis---	9
Db	3801	TTGCGCTAGTCTTCAGTAAATTTCTAAATATATAACACCTGTATCCTGTGAACAAGCATTCG		3860
QY	9		-----	9
Db	3861	TTTAAATTAAGGAAGAAATTATTTGCTCAATTACATTTGTGTAATATAACATAAAAGGAAA		3920
QY	9		-----	9
Db	3921	AGAAATGCTAAGATTGAGAGGTTAATTTCATGTGACCTTTATTTTACTGTGTTTCAG		3980
QY	10		-----Asn-----	10
Db	3981	AAGGCAGATACTATGAGAGAAAAACATATCTCAATTAAAGAGAGAGAGGCATCTTAG		4040
QY	11	Ser	-----IleSer-----	13
Db	4041	TTTTTCTTTGTTTCATAGTCTTAGGGAAGTGTATATCAACAATGAAAAAATGCTTT		4100
QY	14	Trp	-----AlaIle-----Phe---	17
Db	4101	GTAGGGAATGGATAATTAAGTAATTTAAAGTATCCTTTTTTTTTTTTTTTTGTGA		4160
QY	17		-----	17
Db	4161	GAGGAGACTTGTCTCTGTGTCGCCAGGCTGAGTGCAGTGCATGATCTCAGTCACTGCA		4220
QY	18	Thr---Gly	-----Leu-----AlaIleLeu---	23
Db	4221	ACCTGTGGTCTCTGGGTTCAAAACGTATCTCTACCTCAGCTCTGTAGTAGCTGCATAAGG		4280
QY	24	Cys	-----LeuPhe-----Gln	27
Db	4281	CGCTGCCACANGCCAGCTATTTTGTATTTTATACAGATGGGTTTCACAGTGTGGCAG		4340
QY	28		-----Gly-----Val-----	29

Db 5415 TTTCATCCAAATTTGGAAGCTCCCTTATTGCTGCTTCTCCCTCATCACTACTCTGGTAAG 5474
Qy 72 SerThrile----- 74
Db 5475 AGTACAATTTAGGCTCCTAAATTTTACAACATAGTGTAAAGCTCTTTGGCCTGTTAATGT 5534
Qy 75 -----LeuTyr----- 76
Db 5535 GCTATTATTATGAATTCCTCTTTACCTATATCTATTGAAAATATACATTTGGCTGGGTG 5594
Qy 76 ----- 76
Db 5595 AGTGGCTCATGCTGTATCCAGCACCTTTGGAGGCCAGCGGGTGGATTGCTCAAGC 5654
Qy 77 -----Ala-----GlyAsnAsp-----Lys----- 81
Db 5655 CCAGGAGTTTACCAGCCCTGGGCAACATGGGGGAACCCCTGTCTTACAAAAAACAGAGTGGG 5714
Qy 82 -----Trp-----CysLeu-----Asp 85
Db 5715 TGTGGTGGCAGCAGCCTCTAGTCAGTCTCAGCTGCTTGAGAGGCTGAGTGGGAAGAT 5774
Qy 86 ---ProArg----- 87
Db 5775 CACCCAGACTAGGAGTTGAGGCTGAGTGAACCCCTGATTGCACCACTGCACATTCAGCC 5834
Qy 88 ---Val-----Val----- 89
Db 5835 TGGGTGACATAGTGAGACCCTGTCTCAATAAACAACAAAAACAACTTTTCAGAAC 5894
Qy 90 Leu-----Leu-----Ser----- 92
Db 5895 TTAGGAATAGAGGCGMACTTCAACTGTGACAGCAGCATCTACAAAAAAATCTATAGCT 5954
Qy 93 -----AsnThr----- 94
Db 5955 AACATTTAATTTGTAACACACTTCAGTTCTCCCTGTGATTGTGAACAAGTATGCTCTCAT 6014
Qy 95 -----Gln 95
Db 6015 ACTTATTCAACATGGAATTTCTAAACAAGAGAAGAAAAAATGATACAGATCAA 6074
Qy 95 -----Val----- 95
Db 6075 AAAGGAAAAGCTGAAACTATCCCTATTGTCAGATGGCATGATTGCTACATATAAATCT 6134
Qy 96 -----Thr-----Gln----- 97
Db 6135 TCAGAAATTTGTAGAAACACTTTTGTAGAACTAATAAGTAAATTCAGCAAGGTTGAAAGATA 6194
Qy 98 -----Tyr-----Ser----- 99
Db 6195 CTAGATAAACATAGAAAAAATAATTTCTATATATTAGTGATTAACACATGACACTG 6254
Qy 100 -----Ile----- 100
Db 6255 AAATTTTAAATATACATTATAAATTTTTTAAAAAAGAACTCTTTGTAATATACA 6314
Qy 101 -----GluIle-----Gln-----Asn-----Val 105
Db 6315 AGTAAAAAAGAAAGTAGCTTTTAGCCCGAAGATGCAAGTTGGTTCAACAAACAAGTC 6374
Qy 106 -----AspVal----- 107
Db 6375 AACTGATGTAATCTACCAATAAAGTACAAABACTGCATATATCATCCATTACAGATCCAGA 6434
Qy 108 -----TyrAsp----- 109
Db 6435 AAAAGCATTTGAAAAAAACTTCAGCTTTTATGATTAAAAAATACTCAACAGTATAGG 6494
Qy 109 ----- 109
Db 6495 AATAAAGGAAACATATTTTAAAAAGGGACATTTTAAAGAAAAAACCCAGCTAATTTTCATCTT 6554

Qy 109 ----- 109
Db 6555 AATGGATGAATGTTTACATCTATCTTAATTTCTAAGGTTTTCATAAATTTATCCAAAC 6614
Qy 110 -----GluGly----- 111
Db 6615 TTGGTGGCTTAAAGTAAATCTCAGATTCTGAAGGCCAGAAATCTGAATCGAGGTGTCAG 6674
Qy 112 -----Pro-----TyrThr----- 114
Db 6675 TAGGGTTGATTTCTCTCGAAGCTGTGAGAGAGATCCATTCCATATATAGTGCTTAGCT 6734
Qy 114 ----- 114
Db 6735 TCTTGTGGCTGCTGGCAATTTTGGCATTCCTTAACCTTTTGGATGCATCATCTCCAGTCTT 6794
Qy 115 -----CysSer----- 116
Db 6795 TGCTCCATCTTTTGTGTTTTTTTATAGTGGAGTGTGTTCTATCAGTCTAG 6854
Qy 117 ---ValGln----- 118
Db 6855 GCTGGAGTGCAGTGGCATAATCTCAGCTCACTGGGCTCTGCTCCAGGTTCAAGGA 6914
Qy 119 ---Thr---Asp----- 120
Db 6915 TTCTCTGCTCGGCCCTCTGAGTAGTTGAGACTACAGGCATGTACCACCATGCCAACT 6974
Qy 121 -----Asn 121
Db 6975 AATTTTGTACTTTTAGTAGAGATGGGTTTCCACATGTTGGCCAGGCTGGTCTCAAAC 7034
Qy 122 ---His-----ProLys----- 124
Db 7035 TCCTGACCTCAGGCGATCCACCAGCCTCAGCCTCCCAAAGTGTGGGATTACAGGCATGA 7094
Qy 125 ---Thr---SerArg-----Val----- 128
Db 7095 GCCACCATGCCAGACTTTGGCTCCCATCTTCACATGGCCTTCCCTCTGTGTCTATGTCT 7154
Qy 128 ----- 128
Db 7155 TCCTTTCTGTCTAAGGACACTCTCATTTAGGATTTAAGACCACCTTAATCCAGGATGA 7214
Qy 129 ---HisIleu----- 130
Db 7215 TTTCTATCTCAAGATCCTTAATTACATTTGCAAGACCCCTTATTCCAAATAAGGTCACAT 7274
Qy 131 -----IleVal----- 132
Db 7275 CTGAAGTCTGGTAGACATGTCTTTTGAGGGCCACTATTCAATTCATTATAGTACACTCT 7334
Qy 133 GlnVal-----Ser----- 135
Db 7335 CAGATCCCTCAAATTCAGGTCTGTCCCATGCATCAAAATACCTTACTTCAATCCAAATC 7394
Qy 136 ---Pro----- 136
Db 7395 CCCCTGAATCAACCTATTCCAGCATCAACCTGTACATCTAATACCTCTTGTAAATATTTT 7454
Qy 137 ---Lys-----IleVal---Glu-----Ile 141
Db 7455 TAACTCAAAAAGTCCCAATCTTATCTAANTCAGGTATGGGTGATCTCTGGGTATGATC 7514
Qy 142 ---SerSer-----Asp----- 144
Db 7515 CATCCTAGGSCATAATTCCTTTCTAGCTGTAGACCTGTGGACTAGAAAACCAACTATCTG 7574
Qy 144 ----- 144
Db 7575 CTCCTCTAAATACAAATGGTGGGACAGCACTGGATAGCAATCCCAATTCCTCAAAAGGGAGAA 7634

Qy 145 -----IleSer-----Ile 147
Db 7635 GGAGGATGAATAAAGGTATCACAGATCCTAAACAGTTTCAAAACCCAGCAGAGAAATC 7694
Qy 148 -----Asn 148
Db 7695 CCATTAGGTTGAAAAGCTTGAGAAATACCTCTGCAGCTTAATCTCTGCTCTCCAGAAT 7754
Qy 149 -----GluGly----- 150
Db 7755 CAGTGTCCACACTCTGGGTCATGGAGGCTCCTTTGGCTGTCCAGAGGGGTACCTCTC 7814
Qy 150 ----- 150
Db 7815 TGCCTCTGCTCTGCACTCTGGCTCTGGTCTGGTTTGGAGTCATTCTTTTCTCTCAAAA 7874
Qy 151 ----- 151
Db 7875 GGTAGCACATGTTTGCAATTGAGTAGCCTATCAGCCTGTTCCTGCCTGTAGAAATTTGA 7934
Qy 152 -----Asn 152
Db 7935 GAATCTAACACCTTTTTCATTTTGTATAGTCTCAGTCTCTTTTATTTCTAAGCCAGCA 7994
Qy 153 ----- 153
Db 7995 ATGTTTCTGCTGTATTAACATCTCAAAATCCTTGTCTATCTCCCATGTCTCATCCCATG 8054
Qy 154 -----Ile-----Ser-----Leu-----Thr----- 156
Db 8055 GAGGTCCATGCCATTAGACAGAGAGATCTGTCTTGATAGATAGACCTATCTATCTCT 8114
Qy 157 -----Cys----- 157
Db 8115 GACGATCCTTCTGGATTAACCCATCTCTATTCCTGGCTTTTGTCTAAGACAGTTGATTA 8174
Qy 158 -----Ile-----AlaThrGly----- 161
Db 8175 CATCCATGAGTCACACACCTAAATCTCTTCAGCAACAGTTGTCCAGTCAGTCCCTTGGCC 8234
Qy 162 ---ArgProGlu-----ProThrVal-----Thr----- 168
Db 8235 CTCTTCCACAGCATGCTTTTCCAAACAGTAGATTGTTACTTAGCATCTCTGCAATCAG 8294
Qy 169 -----Trp----- 169
Db 8295 GATAGATGAGACTCTTGAAAATCATCAAGTGTGGTGTCTTTTGTCTTAATAACCTCTT 8354
Qy 170 Arg-----His----- 171
Db 8355 CAATTTATCTCTTCTCTCCTCCTCACAATTTTACTTAAGCAGCAAGAGAAATCAGGCTGGCC 8414
Qy 172 -----IleSer-----Pro-----Lys----- 175
Db 8415 TTCAACACTTGTACTTGAATAATCTCAGTTAAATATCCAAAGTTTCATAGCTTANTAAGTTC 8474
Qy 175 ----- 175
Db 8475 GTTTTACCCACAGTAAACATACTTAAGTGGTNTTCTGGTNTGNTGGTTGA 8534
Qy 176 -----AlaVal----- 177
Db 8535 GACTGAGTCTCGCTCTGTCCACCGGCTAGAGTGCAGTGTGCTATCTCAGCTCACTGCA 8594
Qy 177 ----- 177
Db 8595 GCCTCCGCTCCAGGTTCAAGCTATTCTCCTGCCTCTCAGTAGCTGGGATTACAGCG 8654
Qy 178 -----GlyPhe----- 179
Db 8655 AGCGCCACACGCGCCAGCTAAATTTTGTATTTTGTAGTAGAGTTGAGGTTTTCACCATGTTG 8714
Qy 180 -----ValSer----- 181

Db 8715 GCAAGGCTGTGCTCGAACTCGAACTCCTGATTTCAAGTGATCCATCTGCCTTGGCCTTCC 8774
Qy 181 ----- 181
Db 8775 GAAGCTCTGGGATTACGAGGTGTGAGCCGCGTGCCTGGCTGTAGTTTTCGTTTTATATGA 8834
Qy 182 Glu----- 182
Db 8835 GAGTTATATCAGATTCAAGAAATCTCTGCTTTTAAAAATATATCTTGGTAAGATTGGAAGT 8894
Qy 183 -----Asp----- 183
Db 8895 TATATCTGTTGTTAGTTTATGAACCTATCTCTTTTGTCTCTGATCTTAAAAATTTTATGT 8954
Qy 184 -----Glu----- 184
Db 8955 TAGCATATTGTGAGAAACAGGGCTCTTTGAATTAGTGCAAAAGTGCTTTTTTTTAAAT 9014
Qy 184 ----- 184
Db 9015 GTAGATAGCTGTGGGTGCTATCTCTCTAGTAACATTTCTCAAAATAATTTGAAAGTAATG 9074
Qy 185 -----TyrLeuGlu----- 187
Db 9075 TATGTTTTTAAGGCTCTCAATATTTAAAGTACTATCTAGAAATAGTAAATCTAAATTTCT 9134
Qy 188 -----Ile-----Gln----- 189
Db 9135 TTATTTCTTAATGTTAGAAATTTTACAGTTGCAATTGAAATGTAGGTCCCATTTATCAGTTT 9194
Qy 190 Gly----- 190
Db 9195 GGATGCTCTGTGATGATTGTTAGTCTTCTGAAATATTTTTTTCAGAGGTTCTCCATTA 9254
Qy 191 -----IleThr----- 192
Db 9255 CTTGAAAGAGTTCTCCATTACTTGGAAAGATAATATTACAGTTGTGTATAGTGTAGATAAC 9314
Qy 192 ----- 192
Db 9315 ATTATTAAATGTCAGTTTAAATTTCTTCTGAAAGCTTTTGGGTAAATCTTTGGAATAATGAT 9374
Qy 193 -----Arg----- 193
Db 9375 TTAGSAAATTAAGACAAATATTGGTTTGCAGTGAATAAAATTTTACAAGATAAATAT 9434
Qy 194 -----Glu-Gln----- 195
Db 9435 CCATCATTTCTTTTTTTTTTTTTTTTCTCATTTTTTTTAGACACAGGGCTCCCTCTGCTGTG 9494
Qy 196 -----SerGln----- 197
Db 9495 CAGACTGGAGTGCAGTGGCGTGATCATAGCTTACTGCAGCCTTGAACCTCTGGGCTCAGG 9554
Qy 197 Asp----- 198
Db 9555 GGATCCTCCCAATTTAGTCTTCTGAGTAGGTGAACATAAGGTGTCTACCATCACACCTG 9614
Qy 199 -----Tyr-----Glu----- 200
Db 9615 GCTCATTTATTTTTTTTTTTTATTTTTTTTGTAGAGACGGGGTTAGCTATGTTGCCCA 9674
Qy 200 ----- 200
Db 9675 GCGTGTCTCAAACTCTCGCCTCAAGTGATCTCTCCTCTTGGCTCCCAAGTGCTGG 9734
Qy 201 -----Cys----- 201
Db 9735 GATTACAGGTGTGAGCCATGCACTGGCTATCATTTCTTAAATGGATTGTTTTT 9794
Qy 202 -----Ser-----Ala----- 203

[illegible]

QY	239	-----GlyThr-----Leu-----	241
Db	10935	ATACAAATTTTGGCCAGGCAAGGTAGCTCATGCCCTATAATCCAGCACTTAGATGGATG	10994
QY	242	-----Gln-----	242
Db	10995	GGTCAC TTGAGCCAGATGTTTGAGACCAGGCTTGCAACATGGTGAGACCCGTGCTCTA	11054
QY	242	-----	242
Db	11055	CAAAAAATACAAAAATTAGCCGGCTTGGTGTGCACACCTATAGTCTCAGTTACTCAGG	11114
QY	243	-----Cys-----Glu-----	244
Db	11115	AGTTGAGGTGGGAACATCAACCGAGACCTGGGAGGGTTGAGGCTGCAGTGAGCCCTGAT	11174
QY	245	-----Ala-----Ser-----	246
Db	11175	GGCGCTTTGCATTCACGATCTGTGACAGCGATACCCCATCTCAGATAATAATAGTAA	11234
QY	247	-----AlaVal-----	248
Db	11235	TACAAATTTAAAGATCGCAGCTTAGCACTAGTTACATAGCATTATATTGTATTAGSTA	11294
QY	248	-----	248
Db	11295	GTATAGTAATCTAGAGATGATTTAAAGAAATATCAGAGATGTGTAGTTATGCAAT	11354
QY	248	-----	248
Db	11355	ATTACCCCATTTTATTATGTAAAGGATTTGAATATCTGTGGCTTTTGGTGTCTGGGTG	11414
QY	249	-----Pro-----Ser-----	250
Db	11415	TGCGGGTATCTTCAGAACCCCATGGATACTCAGGAGGACTGTACTCTGTAATTTGTG	11474
QY	251	-----Ala-----GluPhe-----	253
Db	11475	TGCATGTGCTTTGTATGTCTTTTTTCTCCAGAGGTGAGAGTTCCTTACTTCATCAG	11534
QY	254	-----Gln-----	254
Db	11535	ATTCTTAAAGGAATGTAGACCAGAAAAAGTTAAAAACATGACCTAACAGGAATTTTG	11594
QY	255	-----Trp-----Tyr-----	256
Db	11595	TTAAAGTGAAGTAGAGGAAAACTGTAAAGATTTTGAACAGTATCTGTGCTGTG	11654
QY	256	-----	256
Db	11655	AATTAAATGTTGTTTCTCTCTTTATTTGTTGGTAATGGAATGAGTTTGTCTTTT	11714
QY	257	-----Lys-----	257
Db	11715	GAGAGAATGATTTTGCTACTTTAACTACTTAAGTTTTTCTTTATTTGTTATGGTTTC	11774
QY	258	-----Asp-----	259
Db	11775	TC TTTTAAATTTGATTTATTGAAGAACTCACATTAAAGATTATCAAAGTCTAGTTGCTTA	11834
QY	259	-----	259
Db	11835	TAAGTAGCTTTGCCCTAATGGGCAATTCGGTATATGTAATTTTATTTGTTTGGAGCTCTTT	11894
QY	260	-----Lys-----	260
Db	11895	GCAATATTTCCAGAGCAATAGATTTTTTTTGTAGATATCACTTAAACGTGCTCAITTTATAG	11954
QY	261	-----Arg-----LeuIle-----	263
Db	11955	ATAAGAGGTTTAGTGCTGTATATTGACTTGTTTAAAGTCATGTTGATTTCCAGTATATA	12014

Qy 264 -Glu----- 264
Db 12015 TGAAGTGTGCCATCTTTTGTGCTGTTTGTGAACCTAAATATTGTCTAATTTTAGATT 12074
Qy 264 ----- 264
Db 12075 ATCAGAGCTATAAACTTCTACTAGTTTCTGTTTTCTTGTCTAGCTTCTCTTCTGGT 12134
Qy 265 -Gly----- 265
Db 12135 CCCTGGCTTCTTTCAGCCTTTGAAACCTCTGGAGCTACTTCTGCCAGGATTAAGCTTTT 12194
Qy 266 -Lys-----Gly-----Val-- 269
Db 12195 TTGTTGAAGTTGTGAGAAATCTGCGCAAGGCCAGAGAGAGAGAGATTAAAGTTAG 12254
Qy 270 -Lys-----Val-----GluAsnArg--Pro-- 275
Db 12255 TCTACCTTTTGGAAATGTTTCAAGAAATGAAATGAGAATAGAAAGTCTCTGAAATCCAG 12314
Qy 276 -----PheLeu--SerLy 279
Db 12315 TCTGGATTAAAAAABACCTCCGTAATAGTTTCTTTTCTTTTCTTTTCTGCAAAAGAA 12374
Qy 279 s-----Leu-----Ile----- 281
Db 12375 AATCTACCTATGTGACGGGGGACACAGAAACATTTCTTGTCTTATCTGTTCTTGGCTA 12434
Qy 282 -Phe----- 282
Db 12435 TTTTGGCTTAAACTCTGTAATACTGTGCTTATTTGTAATATGTAACAGTAATAGTG 12494
Qy 283 -----ph 283
Db 12495 GGAGTTGAATACTGAGGGAAGTAACCGAGTCCATATACCTTCTAGACATAACTT 12554
Qy 283 e-----Asn----- 284
Db 12555 TTACGTAGTGTCTTGTAGCGAGATGCAAAATTAGTTATCTCTAATCACATTACAAG 12614
Qy 285 -----ValSer-- 286
Db 12615 TACTTCCAGTCATACATATGTTAATTTGTTAATTTAAACGACTGGAAAGTCTCTG 12674
Qy 286 ----- 286
Db 12675 GTTGACGACATCTTCTATGTTAAATGGCATTTATGTTAGTAGCAGTAGTAATATCA 12734
Qy 286 ----- 286
Db 12735 TATGTTTGGTTGGGGCTAAGACATGGCCTTCTCACTCAGACCTGGGTTTGAGTCTTGC 12794
Qy 287 -----Glu-----His-----As 289
Db 12795 CTCTGACATTTACTATGAGACCATTAAGCAGTTAATAGCAATTTTTCACAACTGGGA 12854
Qy 289 pTyr----- 290
Db 12855 TTACTTGGCAAGAATATGAAATATATATTTTATCTCTAGAAATGAATTCCTTAGCTG 12914
Qy 291 -----Gly----- 291
Db 12915 GTTTTGAATGGTTATTCAGTCTCTGTTTGAAGAGTGTAGAGCTTATAGCTTCAACT 12974
Qy 292 -----Asn-----Tyr-----Thr----- 294
Db 12975 TTTCTCTCATCTTCTGAACTGATATTTTCTTAGTCTCTTACTGACACAGATTT 13034
Qy 295 -Cys-----Valala----- 297
Db 13035 AATTGCAACAGACTGTGGCTTCCAGAAAGTAGAATCTTGTAGTATATTTTCCATTG 13094
Qy 298 -----SerAsn----- 299

Db 13095 ACACAAGGAATGTACTGTGACTTCTTGTGCTGCCACTGTCTAAAGCTAATGGAAC 13154
Qy 300 -----Lys-----LeuGly-----His----- 303
Db 13155 TTGATGAACATTTCTCTFACCCAGGAAGGATAACAATCTTTGGATATATACCACCTTTGCAGA 13214
Qy 304 -----Thr-- 304
Db 13215 AGCTGTGACTTATGCTGTGGCATATGAGGCCCTGGAGCTAAGAGTCAAGTAGTTAGACTTTC 13274
Qy 305 -----Asn----- 305
Db 13275 TCTTTTGGTTTGTCTTTAATTCAGATCTGTGTAAATCTTTTAGCTTTTGTATGCTT 13334
Qy 305 ----- 305
Db 13335 AGTTGTGTTTTCACATATCCCTCACAAAGATACAGATAACTGATCTGTATCATTAAGTCTA 13394
Qy 306 -----Ala-----Se 307
Db 13395 CAGGTTTATTTATTTGGGGCCAGTCATGTGTGTGTGTCAGCATAGAGTGGCAGTCAACAGTC 13454
Qy 307 r-----IleMet-----LeuPhe--Gly----- 312
Db 13455 AGTAGTAACCTGGATACTGCCACACATAAGTATATCTCCCTTGTTTAGAGGTTTCTTATTA 13514
Qy 313 -----Pro----- 313
Db 13515 TCTGAGTAGGATGATGAAGTTGGTAGTTTCCCTTGTCTCACTTAAGGACTCAAAAT 13574
Qy 313 ----- 313
Db 13575 TTTTCTGTCTGTCTTAGGAAATTAATTGACATTTCTTGTCTTCTGTCTGAGGGCACTC 13634
Qy 313 ----- 313
Db 13635 GGAGAATTAAAGTAGTCTCTTTTATAAGAATGTGATGAATTTAGTTAGAGTTGATATGTG 13694
Qy 314 -Gly-----Ala--Val-----SerGluVal-----SerAsnGlyThr-- 323
Db 13695 TTCAAGACTGAGAGCTGGGTTATGCAAAAGTCTGAGGTTTGTAGTTGACTTAATGGGCACT 13754
Qy 324 -----Ser----- 324
Db 13755 AGATTAAATAAATTTGGATGAATTCAGTAGCTGGAACCCCTTTGGCAAGCAGAGGTTGAA 13814
Qy 325 -----ArgArg-----Ala----- 327
Db 13815 ACATCTTGGAGAAGATGAAAAAATCTAGCCTGGCAGATGAGAACCCAGGGAATGAGTA 13874
Qy 327 ----- 327
Db 13875 CCAGTGAAGGAATATGTCTTGTCAAGGGACAGACAGTAAAGAAATTGAGGAAACAGGCT 13934
Qy 328 -Gly-----Cys----- 329
Db 13935 GGGCAAGTGGCCCAACCTGTAAATCCAGTGTGTTTGGAGGCTGAGGTAGGAAGATCAC 13994
Qy 329 ----- 329
Db 13995 TTGAGCCAGGAGTTCAATACCAGCCTGGCAACATAGCGAGATCCCATCTTTATGAAAA 14054
Qy 330 -----Val----- 330
Db 14055 GTTAAAAAAGTAGCTGAGCGTGTCTAGTCTGTAGTCTTAGTCTTGGAGGCTGAC 14114
Qy 331 -Trp-----Leu-----Leu-----Pr 334
Db 14115 ATGGAGGATCTGAGCCTTAGGAGTTTGGAGTTACAGTGAGCCATGAGTCACTGAGCC 14174
Qy 334 oLeu-----Leu----- 336

Db 1315 GTAAAGATAGACCTGTGTAGTACTAAGTCTCATATAAATATAAGCTATTACAAATTAAT 1374
QY 48 -----Arg-----
Db 1375 TCCATCTCTAGGGAATGTTTTCTTAGGATTCGTGTGAGCTGGTGAATCCCTATCTGT 1434
QY 49 -----Gln-----
Db 1435 TGGGTCTTAACAAGAGTAGAAGCTGGTCAGAAAGAGTGTATTCTGAGAGTAAGAGT 1494
QY 50 -----Gly-----SerAlaThr-----
Db 1495 TTTGGGAAGACTACGATGAGTGTAGTATCTTAATCCAACTCCAACTCCTCACTTGAAGTGAA 1554
QY 55 -----LeuArg-----Cys-----
Db 1555 GGAACCCCTTAGATATGCTGTGTACCTTGGCTGACCAAGTACCTTAATAAACCTCACTTAAA 1614
QY 58 -----Thr-----
Db 1615 GGAGTTAGTTACCTTGCAAAAGAACCCATATGCCCTATCCCTACAAATCCCTCATTTGT 1674
QY 59 -----Ile-----As 60
Db 1675 TCCAGGACACAGTTTGAGTCAGATCCCGAGCATGTCCAGGGAGACAAATACAAAGTGTGA 1734
QY 60 p-----AsnAr 62
Db 1735 TCTGAAGAGCTTTTTTGGATCTTAATATGATAGTGGAGAAATATCTGTGGAATAG 1794
QY 62 g-----Val-----
Db 1795 ATTCTGAATATAGGACCTTGGAGAAGAGACATAAATTTGGTCAATGATCACTATGG 1854
QY 64 -----Thr-----Val-- 66
Db 1855 GTAAACCTATAGTAGAGATTTTGGCTCAGTCTATGAGACTGAACAGCTTGAAGTAGTCT 1914
QY 67 -----AlaTIPLeu-----
Db 1915 TTTTACTGTGTGAACACATTTTGACTCAGCAGTGGCTCATCTAAATTTAGAGATGATAT 1974
QY 70 -----Asn----- 70
Db 1975 GCAGAAACTCCTTGTGTATGATGTAGAGAAAGAAATCAAAGAGAGGGCCCATGTTGG 2034
QY 71 Arg-----SerThr-----Ile-----Le 75
Db 2035 GAGGATTTAATATGAGTGTATCTCTAACTGTATCCCTCGTAAGAGTCTAGTCAACTCTCT 2094
QY 75 uTyraIaGly-----
Db 2095 TTACCAAGGCATTGAGAAAACACTGGTGAGCAGACACCAGCACCTCTGAAAAGCCATA 2154
QY 78 ----- 78
Db 2155 TAGTCTGTGTAGGCCAGAGATGCCAGTGGGAGATGCTTCAGTTGAATGGACCCCTTG 2214
QY 78 ----- 78
Db 2215 ATTGATAGGCATTTTCAAGCTGCGCATGTGTGAGAGACAAAGTAGTGCAATTTAATTTGCT 2274
QY 79 -----Asn----- 80
Db 2275 AGACTAGAAAGGTGGGCATGTTCTCTGTAATAGACAGCAGGAACACAGGATTAATCAGTA 2334
QY 81 -----LysTr 82
Db 2335 TACTCTCAACATGAGTCTGGCTTTGGCTGAAGGATCATGTGATCTAAAGAGGAAATG 2394
QY 82 p-----Cys-----LeuAspPro----- 86

Db 2395 GATAGTCTATTGCTGTATGTTACTATAAACTGTTAGTCTGACTTGAGCCACTGTAGTA 2454
QY 87 -----Ar 87
Db 2455 ATCATGAGCCCTTAACGTATCTCAGGTCTGATTTAATTCAATTTCTGGAGGCCCTGGAG 2514
QY 87 g-----Va 88
Db 2515 AAAGGACTTTGACATANAATCATGAGTATGTATTAATGTATCTCTAGCATTTCTCCAAGT 2574
QY 88 lVal-----Leu-----Ser-----Asn-----Thr----- 94
Db 2575 AATCTGTGGCCATTTACCAGAGCAGTTACAGTGTGAGAAAGAAATTCCTAGACCTTCG 2634
QY 95 -----GlnThr-----Gln----- 97
Db 2635 GGCTCACCAACATGCTGAATTTAGTCTTAATTTTGGCAACCAAGACATCAAAACACTTAT 2694
QY 98 -----Tyr-----Ser-----IleGlu----- 101
Db 2695 TCAGAGTGGAGTCTTGTGGAAGTCAAGTATAAGTGGAGTTTGGACCAAGTCCACACAGT 2754
QY 102 -----Ile----- 102
Db 2755 GACCCCTAAACCCATCCCTTGGTTACTTCTCCCATTTCTCGAGTGTATGGCTAGAGTATT 2814
QY 103 ----- 103
Db 2815 AACATTAGCAACTAGCAGAGTCAACACACTGGTTCTTAACTCGTCTCTTTGTTATCA 2874
QY 103 n-----Asn----- 104
Db 2875 AGTTTAAAGAAAGGATACAACTGATGTACTTTTCAACATGATAAACATTTGCAATGTC 2934
QY 104 ----- 104
Db 2935 CCAAATTTACTACTATTGTTACGAGAAATAGATTGCTCAGTGTGCTTAAAGGAATTTTAA 2994
QY 105 -----ValaspValTyr--Asp----- 109
Db 2995 AGTATTTCTCTTTTGGTTGATGTAGTACCTGATCAGAGTCTTAAACTACCGCTACCAA 3054
QY 110 -----Glu-----Gly-- 111
Db 3055 ATTTTCTTTGAAATCTACCTTTATATGTGAATTAATATACATATATTTTAGGTAA 3114
QY 112 -----Pro----- 112
Db 3115 CAGTAATTTACAGGTTTCTTTTAAATTAAGTATCTTTGCAATTAAGCCCAACTCCTACT 3174
QY 112 ----- 112
Db 3175 GATCAACATTTTCATGCTGATGAAGCATTTAGCAAAATTTGAGACTGATATTCAATTAATA 3234
QY 113 -----Tyr----- 113
Db 3235 TGTATTAAATCAGATAATCTGAGTGTAAATAGTTTGCTCTCTGATTTATAGTAATTN 3294
QY 114 -----Thr-----Cys-----Ser-- 116
Db 3295 TTAATTTGAAAAAACCTCATTTATTCTGCTCATTTTGAAGTTTAAATTTAACTTGGCAAG 3354
QY 117 -Val-----Gln----- 118
Db 3355 AATTACAGCAGCAATTTTNTAATGGTCATTATAGAAACTAGCTNGCATTCACTTAT 3414
QY 119 -----Thr-----Asp-----Asn----- 121
Db 3415 TCTTGATTTACTCTGAATTTATGACCATTAATTAATGAGAAATGAAATNACTCTCTTGT 3474
QY 121 ----- 121
Db 3475 GATAGCTGTACTAGCAGAGAGAAATNTCTTCAATTTCTGCAAAATTAATATTCTCTAT 3534

QY 122 His-----Pro-----LysThrSer----- 126
Db 3535 TCATCTAATGCCTATCCACTAGATTTTGTGTATATG---TCACAGAAGTACTTTTTCCT 3591
QY 127 Arg-----Val----- 128
Db 3592 TAGGTAGTATATTTAAACCTTTTCAGTTATAATTTATACACCCCTCCACCCCTTCCCC 3651
QY 129 HisLeu----- 130
Db 3652 CCACCTTAATGGTTATAAAAGTTACATCCCTTTAAGAAATATTTAGGATAAATATATGATC 3711
QY 131 -----ValGln----- 133
Db 3712 AAATCCTTGAGACAAAACCCAAACCTTTATACAAATCCTTTCATCCAAATCTTATATTT 3771
QY 133 ----- 133
Db 3772 CAAATGAAGTGAGAAATTCATTAGGAAACAATAATTTTTTTTCAACTAATTTTATAG 3831
QY 134 ---ValSer-----ProLysIle 138
Db 3832 TTACATCAGCCTGGGCTAATTAACAGAAATTTATACAAATPACACAAACCAAAAT 3891
QY 138 e-----Val----- 139
Db 3892 ACCAAACCAAGCAACACAAAACCAACCCCAACCAACCAACCTCTCATTCATAAGG 3951
QY 140 -----Glu-----Ile----- 141
Db 3952 TGACAAATTTTACTCTGAGAGGTAGTACAAACCAACCAATGAATCTAGTGCATTA 4011
QY 142 -----SerSer--- 143
Db 4012 ACTGAGGCACCTTAAGATCACCACCTTTTAAATTTATAACCAAAATCTCTCTCTCAGG 4071
QY 144 -----Asp-----Ile----- 145
Db 4072 ATTTGAGTCTCATGAACAAGTATATATAGATTAATGGTCAATTTATCTGACAAA 4131
QY 145 ----- 145
Db 4132 ATCTTACTTTGAAGTTTAGTCATTTAGACCTTAAAGTTACAAAATAAAGTATTTCTATC 4191
QY 146 -----SerIle----- 147
Db 4192 TCAGCAAGTATTTAAATTTCTTAAAGCTAGTAAGAAATGAAGATCAATGTGGAGAGA 4251
QY 148 -----Asn----- 148
Db 4252 AGTATGATTTCTTAAAAATGGGTACATATTTTAGTTTAAATTTCTGAAATACATTATGA 4311
QY 149 -----Glu-----Gly-----Asn----- 151
Db 4312 CCTGTAAGAACATTTCTTCTCTATTTCTATTCAGGGTCATTTTAAACATGTGAGCCTTCAG 4371
QY 152 -----Asn-----IleSerLeu----- 155
Db 4372 CTTTCATTTGTACACTACAAACAGGAAACATAAATCATCATGATCAGTTTGGCAGAGA 4431
QY 156 -----Thr----- 156
Db 4432 TGTGATTAAGAATTGTAAAGATGGCTTTTACATACATACATAAAATTTCCAAACACTTTGC 4491
QY 157 -Cys-----Ile-----AlaThrGly-----Arg----- 162
Db 4492 ATGTGAAAATTTCTGAAATTTAAGCAGTAGGGTGTCTCAGTGAGACTTTGGCTTCATA 4551
QY 163 -----Pro-----Glu----- 164
Db 4552 TGAATGTTTCCATTAATTTTAAAGTTTGGCTTAAACCAAAAACCACTTTGGAAAGCAA 4611

QY 165 -----Pro-----ThrVal-- 167
Db 4612 AGCTCCCAACCAAGCTAAGTTAGAAACTGCTCAGTTTCTGAATGAAAATGACACTGTTT 4671
QY 168 -----Thr-----Trp----- 169
Db 4672 TTATTTTACTCTACTGATTTGAAAGAACAGAAAAGAACTACAGTTGGTATAGAAACT 4731
QY 170 -----ArgHis----- 171
Db 4732 ATTAGGCATCTATACAGACACCTGAGAACCAATTTCTTCTCTACGTTTACCATCTTCGC 4791
QY 171 ----- 171
Db 4792 AGCCACTTGTCTTCTGCTTTTGTCACTCACTGACATTTCAACTCTTTTCAGTTACTGTATCTT 4851
QY 171 ----- 171
Db 4852 CAGATGCTGACTGGACATGGCTTTCTGACTGCTCTCCAGTGTAGGTGGGGTGTGTACT 4911
QY 172 -----Ile----- 172
Db 4912 TTTAAAGGATAGATTTTAAACTGCATCAGAGGTGCATCTGCTGACACCCATTGGGTCAA 4971
QY 173 -----Ser-----Pr 174
Db 4972 AATGAGTTGGCTTACTCGAAAGCCTGTTGAGATAAATAGCACAAAACCTTTTAAACC 5031
QY 174 o----- 174
Db 5032 TGCAAAAGGAAAGAAAGAAAATAATCAGGTTCTTGTTATTTTATTTAAATCACAAT 5091
QY 175 -----Lys----- 175
Db 5092 ATTATTAATAATAATAATATATATATCTTGTCTTCTGCTGCTTCTTCTTGGCATAT 5151
QY 176 -----AlaVal-----Gly-----Phe----- 179
Db 5152 TCATTCCTTTAATGCTGTGCTGTGAATGTTGTAATAAAGGAGGATGTTTCAGTACTGA 5211
QY 180 -ValSer-----GluAsp----- 183
Db 5212 CATCAGTCTTTGCTTCTTGCTAAATTTGTGATCATTTTCATTACTTTCTCTTCTCTG 5271
QY 184 -----Glu----- 184
Db 5272 CAACATACACATACAAAGTTAGCATGCTCTTAAAAATTACAAGCCAAATACCTTTATAAC 5331
QY 185 ---TyrLeu---Glu-----IleGlnGly-- 190
Db 5332 TATATATTTATCTCAAGTATAAATCCTGACACATTTTCAACCTGACTATCCAAATCTTA 5391
QY 190 ----- 190
Db 5392 ATCTTATAATTTATTTCTATTTTTCACGGTCTTCACTTATGTAATTTTTCATATTAAACTG 5451
QY 191 ---Ile-----Thr-----Arg----- 193
Db 5452 CTGAATCAGAACTTCTCTTCTCACTTCAACTCTTCAAGCCACACTCTATTTCGTCTCCT 5511
QY 194 ---Glu-----GlnSerGly----- 197
Db 5512 GTAGGAAGCCATCTGTCAATCTGGGGCTAGTCATCTCATACATTTTCATTTGTTAATAC 5571
QY 197 ----- 197
Db 5572 TACACTACACTACTCAGAGTTTGTATTAAGTTGTCAATTTTTTTTCTTTCTTATAGTCC 5631
QY 198 -----Asp----- 198
Db 5632 TTAATGTGTAAAGTCTTTCTCCCAAGTTATATTCTAAGTTCTTAAGGACAAATGTCTT 5691
QY 199 -----TyrGluCys----- 201

Db 5692 TCATTTTATACCTGTAATTTCTACTAGTGATCAGTATTTGGATACACAGTGGGCTTTAG 5751
QY 201 -----
Db 5752 TAATCAAAAACAAAGAAAAACAACAAGTCTTGAGAGTTTGGACACAGAACTGACA 5811
QY 202 -----
Db 5812 TAAGGTCAATGTTATGATCTCATTTGCTATTTCTCATCACAGCACTTAGTTTTCATTT 5871
QY 203 -----
Db 5872 TGAAGTGAAGAGCCAGCTAAGATTTCTAGAACTGTATCTCTCCAAAAATCACAACATGA 5931
QY 205 -----
Db 5932 AARCACTGAGATACCAATACATATATATGAGATTTTGCCTGGTGTTCACCCCTTGATTAT 5991
QY 211 -----
Db 5992 TTATATATGAAGTTATGGTCAATCTTATCTCTTCAGGGAAGTAAATTAACATCTGCTT 6051
QY 213 -----
Db 6052 AAGCAAAATATTCAGAAAGCTGCCAGGAGCAGTAGCGTACACCTGTGTAACTGGGACCCAA 6111
QY 216 s-----
Db 6112 GTCCAGCTACTTGGGAGGCTGAGGTGGCAGGATGGCTTGAGCCTAGGATTTGAGTCTA 6171
QY 218 -----
Db 6172 GCCTGAGCAACACAGTGAGACCTGTCTCTTAAAAAAGAAAGTATTGAAGGCAAG 6231
QY 219 -----
Db 6232 TTGATACATAAAATAAATTAACATTTCAAAATAAATAAATAAATTAATGTGCACTGTGCTT 6291
QY 222 -----
Db 6292 CTTTACATRAAAACATAAAGCAAAAGGACAACTGGGATCCATCCATCAAAATCAGAAAT 6351
QY 222 -----
Db 6352 ATAAATTTGAAATCTAAAAATTTGAAACTGCATGAAATCTAATGAGGACCTAGTCAAGGA 6411
QY 223 -----
Db 6412 TAGATATCCAGATTAGTACAAGTTCTAGGAGCATCTGAGGCAAAAAAATCTGATGAATA 6471
QY 224 rle-----
Db 6472 CGTTAATAGTGATATCATCAGCAGTATATAGATTTTCTTATCCGATTAAGGGTATATGTGTAGTTGT 6531
QY 228 -----
Db 6532 CTTTTTAAAAATAAATTTCAACTTTCTTATCCGATTAAGGGTATATGTGTAGTTGT 6591
QY 231 -Thr-----
Db 6592 TACGTGGTATATGTGTATGTATGTGGGTTTGGGGTCTTAAACACCCAGCACCCATGCA 6651
QY 234 -----
Db 6652 GTGGCATAGTACCCACAGGTGTTCTTCAGGCCAGGCCACATCCATCCCTCCCCAT 6711
QY 238 -----
Db 6712 CTAGTAGTCCCCAGTGTCTATTATTCCTCATCTGATGTCTGTGAGTACCCAAAGTTTAGCT 6771
QY 239 -----

Db 6772 CCACCTTGTAAGTTAGAACATGGGGCTTTGGTTTTCTGTTCTTGCAATAGTTTATTAGG 6831
QY 239 Y-----
Db 6832 ATAAAGCGCTAGAGTGCCATCCATGTGTGCTGCAAGAGCATGATTTTGTCTTCTTTATG 6891
QY 243 -----
Db 6892 GCTGCATAGTATTCCTTTAGTACATATGTTTCATTTCTTTATCCAGTCCATGTATGATGG 6951
QY 244 -----
Db 6952 CACCTAGTTGATCTGTCTTTGCTACTGTGTAATAGCACCTGCAATGACATATAACGTAT 7011
QY 248 l-----
Db 7012 CTTTGACAGATGAATTAATTTCTTTGGGTTTGCATAGTACTCATTTTAAAGATTTTA 7071
QY 249 -----
Db 7072 TGTGTTGACCAATGGTCTTAGAATAACCATATAATTTAAAGTTATAGAGAGCCACAA 7131
QY 250 -----
Db 7132 AAATTAGTCTAAATTTCTTTAAATTTACTTATGAGAAAGGCTCACAGATTAATAACAAATTT 7191
QY 252 -----
Db 7192 TTTTTTGGAGATGGAGTTTGGCTGTGTGCCCAGGCTCACAAATCCTTACACTATCCTC 7251
QY 255 -----
Db 7252 CCACCTCAGCTCCTCAGTAGTGAGATTACAGGTGTGTGCTACTGTGCTCTTTGGCTTTT 7311
QY 256 -----
Db 7312 GAAATATTTTAAAGCTTATTATGTTTACTTTTACTTTTCTTAAAGAGATTTAAGATAATT 7371
QY 258 -----
Db 7372 TTGCTGAATGGGAGGACCTGGCTGAGTTTATATAACAAGCTGCTGATAGGATAACTC 7431
QY 259 -----
Db 7432 TTAAATCTAATTTTTTTTTTTTTTTTTTTTTTTTGTGAGACAGTCTGATCTGTACCCAGGCT 7491
QY 261 -----
Db 7492 GGAGTGCAGTGGTCAATCTTGGCTAACTGCAGCTGCTGCTCTGGGTTTCAGGCAATTC 7551
QY 262 -----
Db 7552 TCCACCTCAGCTCTCAAGTAGTGGTATTACAGCTTGCATGACACACCTGGCTAAT 7611
QY 263 e-----
Db 7612 TTTTGTGTTTTTGTAGACAGGGGTTTCCACCATGTGTGGCCAGGCTGGTCTTGAACCTCT 7671
QY 267 -----
Db 7672 GACCTCAAGTATCTACCCAACTTGGCCCTCCCAAAATGTGGGATTTATAGGATAGCCA 7731
QY 268 -----
Db 7732 CTATGCCAGCAAACTAATATCTTTATAGTATCAATGCTTCTTTGTCTTTCCCTC 7791
QY 269 -----
Db 7792 CAACAGAGAAATAGTAGAATGATCAATTTAAGTTATCAAAATTTAGTTGAAGATGCCAA 7851
QY 272 -----
Db 7852 ATGAACATGGCTGTGTCAGAGATGATGAGTATTTTAAACTATATATATAAAGA 7911

QY 272 ----- 272
Db 7912 AATTTAAGTTCTCTGCTTTGAAGTCAACATAAAGCTGAGCAACTAATAAAAAAT 7971
QY 273 -----PheLeuSe 278
Db 7972 TACAGTGATATAAAGGCCACTGCTCTTCAAACTTAACACTCTACAGTCTTCTTTTC 8031
QY 278 r-----Lys----- 279
Db 8032 ATCTGCTACTCAAAAACACATCTAGAACTTAAAGTTTTTAAAAAGCAAAACAACTT 8091
QY 280 -----LeuIlePhe-----PheAsn-----ValSer--- 286
Db 8092 AGACATTAGGCGCACTGAATTTTAAATCTTAACATCCCTTTAATGAATTTAGTGTCTAC 8151
QY 286 ----- 286
Db 8152 CACAGCTAGATTTAAAGTATGCACATATCCTAAATTTATATGAAGGCCATATAAAT 8211
QY 286 ----- 286
Db 8212 CTTTGGCTGAAGATGAGGCTCTCTGCTTACTTAAATGAATTCGTATATATATAT 8271
QY 287 -----Glu----- 287
Db 8272 TAATGAGCAATTTTAAAGAAATTAGATAAAATTTTATCTTAACTATAAATTAATAT 8331
QY 288 -----His----- 288
Db 8332 AACTTTATCATATAAATTTGATCTTATTTATTCACATGGTTCAAGATCATACAGTTCTG 8391
QY 289 -----Asp-----Tyr----- 290
Db 8392 TTCAAAGGATNAACATATATTACAGATGTGAACAAAGCATATGTAAACAGAAATTCCT 8451
QY 291 -----Gly----- 292
Db 8452 ATGTGTGAATGCTGATACAAAGTTTACTACAGTTTGTGTGTCATATAATGAATGT 8511
QY 292 ----- 292
Db 8512 ATTTTAAAGTGGCTACCATGCAATCTCTCTCTCTACCCCTTTGCTATATGCTCTT 8571
QY 293 -----Thr-----Cys----- 295
Db 8572 TTGACCTGATGTACATATGTACACATATATGCATACATACCTTGTGCAATGAAT 8631
QY 296 -----ValAlaSer----- 298
Db 8632 ATCTGTTGCTGTCATCTGTAGTTTAAATAATACACATTTCTTCTTAAATAAAG 8691
QY 299 -----Leu----- 300
Db 8692 CAATGGGAAAGAAAATATTTTACAGATGACATATAAGCAACACTCAGTTTAAATAAA 8751
QY 300 s-----Leu-----Gly----- 302
Db 8752 AGTTTATGAATTTCCATCCACACTATTTTCAGGAATATGCAAGATTTCTGTGGCCAAAC 8811
QY 303 -----His-----ThrAsn----- 305
Db 8812 TGAAGTCAAAAATTAATTTTAAACCCTCTATAATAGCAGTTTCTAATTTATATGAGA 8871
QY 306 -----Ala-----Ser---Ile----- 308
Db 8872 ACCTAGGATATTCATAGGCTCATATCAATAGTCAGATACAACTACAAAATTTGGCTGT 8931
QY 309 -----Met----- 309
Db 8932 TGTTACTAAACAGAAAAACACATAGCTTTTACTGAATGAAGATATAAATGTAGTTCTGT 8991

QY 310 -----Leu-----Phe 311
Db 8992 GTCTTATAGATATTACAAATTTTGGCCACAACACTCTCTGAATTTACCAAAAGTTCTTT 9051
QY 311 e-----GlyPro----- 313
Db 9052 TTCTAGAAGCACATCTAGGGTAATAAAAAATCAAAAGGACCTTTAGTGTACTTTGTTC 9111
QY 313 ----- 313
Db 9112 TTTTAAAAATCTAGTAAATTTAAAAACACACAAAAAGAGGTATCTTTAAAAAAA 9171
QY 314 -----GlyAlaVal-----Ser-----Gly 318
Db 9172 TTATCAGGGCAATGGTGGTTTCATGCTGTAAATCCAGCCACTTTGGGAGGTCAAGGTGGGA 9231
QY 318 u-----ValSer-----Asn-----Gly-----Thr----- 323
Db 9232 GGACTGCTTGAGCCAGGAGTTTGAATCCGCTGGACAATATGTTGAGACCCCATCTCT 9291
QY 324 -----Ser-----ArgArg----- 326
Db 9292 AAAAAATATTAGCCAGGTGGTGTGTCATCTTGTGTCCTCCAGCTACACAGGAGTTGAG 9351
QY 327 -----AlaGly----- 329
Db 9352 GCTGAGCAAGAGACTGCTGCTGAGTCTAGGAGGTTGAGACTGTCAGTGAGCCATGTTGTG 9411
QY 329 s----- 329
Db 9412 CCACCTGTATTCAGCTTGGGTGAAAAGTGAGACCAGTATCCAAAAAAAACAA 9471
QY 329 ----- 329
Db 9472 AACCAACAACACTATTTCATCATTCACCTATTTCATCTCAGGCTGATTACAGCCTGATA 9531
QY 329 ----- 329
Db 9532 AAATCTGTAAATTTAAAAAAAACAGAGGATCAGACTCATTTAGAGAGATTTACTAAAAA 9591
QY 330 -----Val----- 330
Db 9592 CACACTATTTATAATTATATGTTTATTATATACATCAATACAAATTTGAAAAAGATACA 9651
QY 331 -----Tyr-----LeuLeu--- 333
Db 9652 GTATTTTGGTAAGCAGCTTTAAAGCTAGTAGCTAGGTTTCAGTTAGTCACTTGTCTGT 9711
QY 333 -----Pro----- 333
Db 9712 TGACATTTGAGATGTCATGAATTTGAAAACCTGACTTTTGAGGGGTACACTCTGATTTCAAAGA 9771
QY 333 ----- 333
Db 9772 TTAATGCTTTTATTAGGCTCTGAATGTATCCAAACCATGTTGAAGAGATTTCAATAGCA 9831
QY 334 ----- 334
Db 9832 TTCTTTTGAAGATCCAGTATTTGAAAAGGGAACCTTGACCTGAAAAGAAAAAGATATACAG 9891
QY 335 -----Leu-----Val-----LeuHis----- 339
Db 9892 AGAAGTGGTTTGAAGAAATGTTCTCTTTTAAAAAGAAAGTCTTTCACAAATTTAACTATAAG 9951
QY 340 -----LeuLeu-----LeuLeuPhe 344
Db 9952 TAAGATATAAATTAATATATATGACAGAGTAATTAATTAATTC 9994

RESULT 28
AY404419

LOCUS

DEFINITION Pan troglodytes LRP1 gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

12485 bp DNA linear

GSS 15-DEC-2003

ACCESSION AY404419
 VERSION AY404419.1 GI:39760396
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 REFERENCE 1 (bases 1 to 12485)
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 12485)
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
 FEATURES
 source
 1..12485
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 gene
 <1..>12485
 /gene="LRP1"
 /locus_tag="HCM1884"
 ORIGIN
 Alignment Scores:
 Pred. No.: 3,76e-12 Length: 12485
 Score: 1665.60 Matches: 292
 Percent Similarity: 9.93% Conservative: 43
 Best Local Similarity: 8.66% Mismatches: 4
 Query Match: 69.17% Indels: 3035
 DB: 29 Gaps: 266
 US-10-017-084a-523 (1-344) x AY404419 (1-12485)
 QY 1 MetLys-----ThrIle-----Gln--- 5
 Db 40 ATCAATACCTGTATCTCAAGGGCTGGCGGTGGCGACGTGAGAGGGACTGCCAGAGC 99
 QY 6 -----ProLysMet-----His----- 9
 Db 100 GATCTGACGAGGCC---CTGAGATTGTCCACAGAGTAAGGCCCGCAGCGATGCCAGCA 156
 QY 10 AsnSerIleSer---TrpAla-----IlePhe----- 17
 Db 157 ACAGCATAACTACCTCGGTGGTACTGAGCTGTGTGTCTCCCATGTCCCGCTCTGCAATGGG 216
 QY 18 -----Thr-----Gly----- 19
 Db 217 TCCAGACTGCATGGAGCGCTCAGATGAGGGGCCCCCACTGCCAGAGTCCCGAGGCAACT 276
 QY 20 ----LeuAla----- 23
 Db 277 GCTCTCGCTGGGCTGCCAGCACCATTGTGTCCCACTCTGATGGGCCCACTGTCTAC- 335
 QY 24 Cys-----Leu-----Phe----- 26
 Db 336 TGCAACAGCAGCTTTCAGCTTTCAGGCAGATGGCAAGCTGCAAGATTTCATGATGATNN 395
 QY 27 -----Gln----- 27
 Db 396 TCAGTGTACGGCNCNNNCAGCCAGCNATGCACCACAGATGGCTCTTCATATATGTGGC 455

QY 28 ----Gly----- 28
 Db 456 TGTGTTGAAGGATACCTCTCTGCAGCCGGATAACCGCTCTCTGCAAGGCCAAGACGACCA 515
 QY 29 Val-----ProVal----- 31
 Db 516 GTAGACCGGCCCTCTGTCTGTGTATAGCACTCCAGAACATCTTGGCCACGTACTGT 575
 QY 32 -----Arg----- 32
 Db 576 AGTGGGGCCCGAGTGTCTACCATCATCAGCCTACGAGCACACGGCAGACACAGCCATGGAC 635
 QY 33 ---Ser-----GlyAsp----- 35
 Db 636 TTCAGCTATGCCAACGAGACCGGTATGCTGGGTGCATGTGCGGGACAAATGCTGCTCAGAC 695
 QY 35 ----- 35
 Db 696 CAGCTCAAGTGTGCCCGCATGCTCTGGCNCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 755
 QY 36 -----Ala-----Thr----- 37
 Db 756 NNN 815
 QY 38 -----Phe----- 38
 Db 816 TACTTTGTGATGACATCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 875
 QY 39 -----ProLys-----Ala----- 41
 Db 876 GTCACATGCTAGACCTGGAACTCTACACCCCAAGGGCATTGCTTCTCAGCGCATCACGCTG 935
 QY 42 -----MetAsp 43
 Db 936 GGGAGGTGTTTTTCACTGACTATGGGCGAGATCCCAAGGTGGAACGCTGTGCATGGAT 995
 QY 44 ---Asn-----ValThr----- 46
 Db 996 GGGCAGAACCGCACCAAGCTCTCGACAGAAAGATTGTGTTTCTCAGCGCATCACGCTG 1055
 QY 47 -----Val 47
 Db 1056 GACCTGCTCAGCGCCTTGTCTACTTCTGCTGCGGCGAGATGCTTCTGAGTATATTGAGTGGTG 1115
 QY 48 -----ArgGln----- 49
 Db 1116 GACTATGAGGGCAAGGGCGCGCAGACCATCATCCAGGGCATCTCTGNNNGAGCACCTGTAC 1175
 QY 50 Gly-----Glu-----Ser-----Ala----- 53
 Db 1176 GGCCTGACCGTGTGTGAGAAATTATCTCTATGCCACCACTCGGACAAATGCCAATGCCAG 1235
 QY 54 -----Thr 54
 Db 1236 CAGAAAGCAGTGTGATCGTGTGAACCGCTTTAAACAGCAGCAGGTACAGGTGTGCACC 1295
 QY 55 -----Leu-----Arg 56
 Db 1296 CCGGTGGACAAGGGTGGTGGCTCCCTCCACATCTACCACAGAGGCGTCAGCCCGAGTGAGG 1355
 QY 57 -----Cys----- 57
 Db 1356 AGCCATGCTGTGAAAAACGACCATGATGGGAAGCGGGTGGCTGTCTGACATCTGCTGTG 1415
 QY 58 -----Thr----- 58
 Db 1416 CTGGCCAAACAGCCACAAGCGCGGACCTGCCGCTGCCGCTTCGGGCTTCAGCTGGGCGAGT 1475
 QY 58 ----- 58
 Db 1476 GACGGGAAGTCATGCAAGAAGCCGAGACGAGCTGTTCTCTGTGTATGGCAAGGCGCGG 1535

QY 59 -----Ile-----Asp----- 60
Db 1536 CCAGGCATCATCGGGGATGATATCGGGGCAAGGTCCCGGATGAGCACATGATCCCC 1595
QY 61 -----Asn----- 61
Db 1596 ATTGAACCTCATGAACCCCGAGCCCTGGACTTCCACGCTGAGACCGGCTTCATCTAC 1655
QY 62 -----Arg-----Val-----Thr-----Arg----- 65
Db 1656 TTGTCGACACACCACAGCTACCTCATTTGCCCGCCAGAGATTGAGCTAGCGGGAG 1715
QY 66 -----ValAla-----TyrLeu----- 69
Db 1716 ACCATCTGAAGAGCGCATCCACATGTGGAGGTGTGGCCGTGGACTGGATGGAGAC 1775
QY 70 Asn----- 70
Db 1776 AATCTGTACTGGACGACGATGGGCCCAAAAGACAATCAGCGTGGCCAGGCTGGAGAA 1835
QY 71 -----Arg-----Ser-----Thr-----Ile----- 74
Db 1836 GCTGCTCAGACCCGCAAGACTTTAATCGAGGGCAAAATGACACACCCAGGGCTATTGTG 1895
QY 75 -----Leu-----Tyr----- 76
Db 1896 GTGGATCCACTCAATGGGTGGATGTACTGGACAGACTGGGAGGAGACCCCAAGGACAGT 1955
QY 77 -----Ala-----Gly----- 78
Db 1956 CGGCGTGGCGGCTGGAGAGCGCTGGATGGTGCCTCACACGAGACATCTTTGTCCAC 2015
QY 79 -----Asn-----Asp-----Lys----- 81
Db 2016 TCCAGACAGTCTTTGGCCCAATGGGTAAAGCTTGGACATCCAGCTGGGGCGCTCTAC 2075
QY 82 Trp----- 82
Db 2076 TGGGTGGATGCTTCTACGCGCATCGAGACGATACTGCTCAATGGCACAGACCGGAAG 2135
QY 83 -----Cys----- 83
Db 2136 ATTGTGTATGAAGTCTTGAGCTGAACACCGCTTTGGCCGTGTGTCACCATGGCACTAC 2195
QY 84 -----LeuAsp----- 85
Db 2196 CTCCTTGGACTGATCGGAGTGGCAGTGTCTACCGCTTGGACAGGGGTGTAGAGGC 2255
QY 86 -----Pro-----Arg-----Val-----Leu----- 90
Db 2256 GGNNNCCCACTGTGACCCCTTTGTGGCAGTGGAGCGGCCCCCATCTTTGAGATCCGAATG 2315
QY 91 Leu-----SerAsn----- 93
Db 2316 TATGATGCCACGACGACGAAGTTGGCACCAACAAATGCCGGTGAACAATGGCGGTGC 2375
QY 94 -----Thr-----Gln-----Thr-----Gln----- 97
Db 2376 AGCAGCTGTGTGTGGCCACCCCTGGAGCGCCGAGTGGCGCTGTGCTGAGGACCAAGTG 2435
QY 98 -----TyrSerIle----- 100
Db 2436 TTGACGACGAGCGGCTCACTGTGTTGGCGAACCCATCTAC--GTGCTCCACCCGAG 2492
QY 101 -----Glu-----IleGln----- 103
Db 2493 TGCCAGCGGGAGTTTGGCTGTGTGCCAACAGCCGCTGCATCCAGGACCGCTGGAGTGT 2552
QY 104 -----Asn-----ValAsp----- 106
Db 2553 GACGAGACAACGATTGCTTGACACAACAGTGTATGAGGCCCGCCCTCTGCCATCAGCAC 2612
QY 107 -----Tyr-----Val----- 108

Db 2613 ACCTGCCCTCGGACCCGATTCAAGTGGAGAACCAACCGGTGCATCCCAACCGCTGGCTC 2672
QY 109 -----AspGlu----- 110
Db 2673 TGGACGGGACAAATGACTGTGGGACAGTGAAGATGAGTCCAATGCCACTTGTTCNNCC 2732
QY 111 -----Gly-----Pro-----Tyr 113
Db 2733 CGCAGCTGCCCGCCCAACACAGTCTCTCTGTGCGAGTGGCGCTGCATCCCACTCTCTGG 2792
QY 114 ThrCys-----Ser----- 116
Db 2793 ACGTGTGATCTGGATGACGACTGTGGGACCGCTCTGTGAGTGTGTCTGTGTGCTTAT 2852
QY 117 -----ValGln-----Thr----- 119
Db 2853 CCCAGCTGCTTCCCGCTGACTCAGTTTACCTTGCACAAATGGCAGATGTATCAACATCAAC 2912
QY 120 -----AspAsn-----His 122
Db 2913 TGGAGATGCGACAATGNNNNNNNNNGTGGGACACACAGTGCAGGAAGCGGCTGCAGCCAC 2972
QY 123 -----ProLys-----Thr 125
Db 2973 TCCTGTTNAGCACCCAGTTCAAGTGCAACAGCGGGGTGTCATCCCGAGCACTGGACC 3032
QY 126 -----Ser----- 126
Db 3033 TGGATGGGACAATGACTGCGGAGACTACAGTGTATGAGACACACGCAACTGCACCAAC 3092
QY 127 -----Arg-----ValHis----- 129
Db 3093 CAGGCCACGAGGCCCTGTGGTGTGCACACATGATGAGTTCCAGTCCCGCTGGATGGA 3152
QY 130 Leu-----ValGln----- 133
Db 3153 CTATGCTATCCCGCTGGCGTGGCGTGGGAGCACTGACTGCTCATGGACTCCAGCAT 3212
QY 134 -----ValSer-----Pro-----Lys 137
Db 3213 GAGAAGAGCTGTGAGGAGTGACCCACGCTGTGTATCCCACTGTCAAAGTTTGGCTGCAAG 3272
QY 138 -----Ile-----Val-----Glu----- 140
Db 3273 GACTCAGCTCGTGCATCAGCAAAAGCGTGGTGTGTATGGCGACAATGACTGTGAGAT 3332
QY 141 IleSerSerAsp-----Ile----- 145
Db 3333 AAC--TCGATGAGGAGAACTGCGAGTCCCTGGSCCTGGAGCCACCCCTGCACCCCTTGT 3389
QY 146 -----SerIle-----Asn----- 148
Db 3390 GCCAACAAACCTCAGCTTCGCTGCGCTGCACAGCTGTGTATGGCAACAGCACTGT 3449
QY 149 -----GluGly-----AsnAsn----- 152
Db 3450 GGGACGGCTCAGATGAGGGGAGAGCTTCGGACCAAGTGTCTCTGAATAACGGTGGCTGC 3509
QY 153 -----Ile-----Ser----- 154
Db 3510 AGCCACAACCTCAGTGGCACCTGGCGAAGGCAATGTGTGTCTCTGCTCTGGGATG 3569
QY 155 -----Leu-----ThrCys-----Ile-----Ala----- 159
Db 3570 GAGCTGGGGCCCGACACCACTGCGAGATCCAGAGCTACTGTGTGCCAAGCATCTCAAA 3629
QY 160 -----Thr----- 160
Db 3630 TGCAGCAAAAGTGGGACGACAGTTCAGCGTGAAGTGTCTCTGTCTACGAGGGCTGG 3689
QY 161 -----Gly-----Arg-----Pro----- 163

Db 3690 GTCTGGAACCTGACGGCAGAGGTGCCGAGCGCTGGNCCCCTTCAAGCGCTTCATCATT 3749
QY 164 -----Glu----- 164
Db 3750 TTCTCCAACCGCATGAATCCGGCGCATCGATCTTCAAAAGAGACTACAGCGCTCTG 3809
QY 165 ---Pro----- 165
Db 3810 GTGCCCGGCTGCGCAACACCATCGCCCTGGAATTCCACCTCAGCAGCGCCCTCTAC 3869
QY 165 ----- 165
Db 3870 TGAACGACGTGTGGAGGACAAGATCTACCGGGGAAGCTGTGGACACGAGCGCCTG 3929
QY 166 Thr-----Val----- 168
Db 3930 ACTAGTTTCAGGTGTGATTACGATGGCTGGCCACACCCAGAGGCCTAGCTGAGNC 3989
QY 169 -----Trp----- 169
Db 3990 TGGATTGAGCANCATCTACTGGTGGAGAGTAACCTGGATCAGATCGAGGTGGCCAAG 4049
QY 170 -----Arg-----His----- 171
Db 4050 CTGGATGGGACCTCCGGACCAACCTCTGTCGCCGTGACATTCAGCACCCAGGGCAATC 4109
QY 171 ----- 171
Db 4110 GCACTGGATCCCGGATGGATCTCTGTTTGGACAGACTGGGATGCCAGCTGCCCGC 4169
QY 172 Ile-----Ser 173
Db 4170 ATTGAGGACGCTCCATGAGTGGGCTGGCGCGCACCGTGCCACCGGAGACCGCTCT 4229
QY 174 -----Pro-----Lys----- 175
Db 4230 GGGGGTGGCCCAACGGGCTCACCGTGGACTACCTGGAGAAGGCATCCTTTGGATTGAC 4289
QY 176 -----Ala-----Val----- 177
Db 4290 GCCAGTCAGATGCCATTACTCAGCCCGTTAGCAGCGGCTCTGGCCACATGAGAGTGCTT 4349
QY 178 Gly-----Phe-----Valser-----Glu----- 182
Db 4350 CGGGGACAGAGTTCCTGTGACCCGCTTTCAGTGACGCTGTACGGGGGGAGGCTCTAC 4409
QY 182 ----- 182
Db 4410 TGGACTGACTGGGGAACAACACACTGGCTAAGGCCAACAGTGGACCGGCCACATATGC 4469
QY 183 -----Asp----- 183
Db 4470 ACGTGGTACAGAGGACCAACACCCAGCCCTTTGACTCGAGGTGTACCACCCCTCCCGC 4529
QY 184 -----Glu----- 184
Db 4530 CAGCCCATGGCTCCCAATCCCTGTGAGGCCAATGGGGCGCGGGCCCTCTCCACCTG 4589
QY 185 -----Tyr----- 185
Db 4590 TGTCTCATCAACTAACCGGACCGGTCTCTGGCCCTGCCGCCACCTCATGAAGCTCCAC 4649
QY 186 -----Leu-----Glu 187
Db 4650 AAGGACACACACANNNNNNNNAGTTTAAGAAGTTCTCTGTATGACGATGGAG 4709
QY 188 IleGlnGly----- 190
Db 4710 ATCCGAGGTGTGACCTGGATGCTCCCTACTACAACTACATCATCTCTTCACGGTGCC 4769
QY 191 -----Thr-----ArgGln----- 195
Db 4770 GACATCGAACAGTCACTAGTGTAGTACTAGGATGCCCGGAGCGGTGTGTACTGGTCT 4829

QY 195 ----- 195
Db 4830 GACGTCCGACACACAGGCCATCAAGCGGCTTTCATCAACGGCACAGGAGTGGAGCAGTC 4889
QY 196 ---Ser----- 196
Db 4890 GTCTCTGACAGNN 4949
QY 196 ----- 196
Db 4950 NNN 5009
QY 196 ----- 196
Db 5010 NNN 5069
QY 197 -----GlyAsp----- 198
Db 5070 NNNNGAAGCTCTACTGGACCGATGGTGACAATCAGCATGGCCAAATGATGGCAGC 5129
QY 198 ----- 198
Db 5130 AATCGCACCTGCTCTTCAATGGCAGAGGGCCAGTGGGCTTGGCTATTGACTTCCCT 5189
QY 199 -----Tyr----- 199
Db 5190 GAAAGCAAACTCTACTGGATCAGCTCCGGGAACCATACCATCAACCGCTGCAACCTGNT 5249
QY 199 ----- 199
Db 5250 GGGNN 5309
QY 200 -----Glu-----Cys 201
Db 5310 NNNNNNNNGGACAAGCTGTGTGGGCAGATCAGGTGTGGAAGAGATGGCACATGC 5369
QY 202 Ser---Ala-----Ser-----Asn----- 205
Db 5370 AGCAAGGTGACGGGTTCGGGCTCCGTGTCCTTCGGAACAGCACACCCTGGTGATGCAC 5429
QY 206 -----Asp-----Val 207
Db 5430 ATGAAGTCTATGACGAGAGCATCCAGCTGGNNNNNNNNNNNNNNNNNNNNNNNGCAGTGC 5489
QY 207 ----- 207
Db 5490 AACAACGGTGACTGCTCCNNNNNNNGCCTGCCACGTCAGAGACGACCGCTCTGTCATG 5549
QY 208 -----Ala----- 208
Db 5550 TGACACGGGTATAGCCTCCGGAGTGGCCAGAGGCTTCGAGGGCGTAGGTTCTCTTT 5609
QY 208 ----- 208
Db 5610 CTCCTGTACTGTGTCATGAGGAATCAGGGAATTCCTCCTGGATCCCAATGACAAGTCA 5669
QY 209 ---Ala-----ProVal----- 211
Db 5670 GATGCCCTGGTCCAGTGTCCGGGACCTCGTGGCTGTGCGCATCGACTTCACCGCTGAA 5729
QY 212 -----Val----- 212
Db 5730 AATGACCACTACTCTGGTGGACATGGGCTTGACACGATCAGCCGGGCCAGCGGAC 5789
QY 213 -----Arg-----ArgValLys-----Val 217
Db 5790 CAGACGTGGCGTGAAGACGTGTGTGACCAATGSCATTGGCCGTGTGGAGGCAATTCAGTG 5849
QY 218 -----Thr-----Val----- 219
Db 5850 GACTGGATCGCAGGCAACATCTACTGGACAGACAGGCGCTTTGATGTATCGAGGTCCGC 5909


```

SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 9567)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE       Inferring nonneutral evolution from human-chimp-mouse orthologous
JOURNAL      Science 302 (5652), 1960-1963 (2003)
PUBMED      14671302
REFERENCE    2 (bases 1 to 9567)
AUTHORS      Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE       Direct Submission
JOURNAL      Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
COMMENT      Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES     Location/Qualifiers
             source
               1..9567
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /db_xref="taxon:10090"
               <1..>9567
               /locus_tag="HCM2081"
ORIGIN
Alignment Scores:
Pred. No.:      1..11e-12      Length:      9567
Score:          1665.50      Matches:    283
Percent Similarity: 11.03%      Conservative: 48
Best Local Similarity: 9.43%      Mismatches: 6
Query Match:    69.17%      Indels:     2666
DB:             29          Gaps:        248
US-10-017-084A-523 (1-344) x AY405011 (1-9567)
Qy      1 MetLys-----Thr-----Ile----- 4
Db      373 ATGGAAGAGTTTCCTCTCCCCACCTGATGTTGTCTAGACACCAATGGATGTGACGCA 432
Qy      5 -----Gln-----ProLys-----Met----- 8
Db      433 TTTTCCAGTCCCTGGAATCCCGCCCTCTAGAGACTGCCAATGCCCAAGATTTA 492
Qy      9 -----His----- 9
Db      493 TACTCCAGCAAGAAATTTATATGAATTAACCGTTTATATAGCATATCCATCCAGAG 552
Qy      9 ----- 9
Db      553 TTAAGAAAAACTTAGAAAAAGATTACATCAGTGAGGTTTCTGAAATGTTTCTAGCCAG 612
Qy      9 ----- 9
Db      613 ATAACTCAGGAACGGTTATCAGCATGTACAAAAGCTCGGTATGTTTTCGAAAT 672
Qy      10 -----AsnSer----- 11
Db      673 ACAATGACAGTTCTCAGAAAGATTGAACTCAGAAAGAGAAAACCTCGAGTGGGATGAA 732
Qy      12 Ile-----Ser-----Trp----- 14
Db      733 ATCTCAAAGGAGAGTGCATCGATTCGATGGATTTTGTGAAATCAGCCATTAGATTCT 792
Qy      15 -----Ala----- 15
Db      793 ATCAACCATGGTTCTACAGATGAAGGTAGACTTCCAAAGGCATTTGACCAAGAACTA 852
Qy      16 Ile-----Phe----- 17
Db      853 ATTCTGGAAGTGTGTAATAATACAACTTTGGATGTTTGAACCTCAGCCAAATAGATGCA 912
Qy      18 -----Thr-----Gly-----LeuAla----- 21
Db      913 CTGGGGATTCTTCTGCTGGCACTGAAGGAAACACTGAGAAAATTCCTGAACTAGCTAGA 972
Qy      22 -----Ala-----Leu----- 23
Db      973 GGAGATGTTTACACAGCAAGGTGGATGTTTGAACAAGGCCCTTTAGACTCCATCAACAAA 1032
Qy      24 -----Cys-----Leu----- 25
Db      1033 ATGCATGAATGTCAGAGAAACAGCATCTACTCTTACAAAGGATATACTGGTGGAGAT 1092
Qy      26 -----Phe----- 26
Db      1093 GTCAGACTGTGAGATACATGTTTGAACCTCAACAACTAGATCACTTGGACAGCTTCAC 1152
Qy      27 -----Gln-----Gly----- 28
Db      1153 TCAGTGGATGAATTGAACCTTGTACAACTCAGATCAGAACTCAAGAAATTTAAAGGAAT 1212
Qy      29 Val-----Pro-----ValArg-----Ser 33
Db      1213 GTTAAGAGAAACATAAAGTGTGTTTGAACCTCAACCATTTGTATGTATGATGATGGTTCA 1272
Qy      34 -----GlyAsp----- 35
Db      1273 GGCCAAATGTAGAAATTTAAACTGTGTCAGAGAGAGACATTTGAAAAGGCGATGTAAAG 1332
Qy      36 ---Ala-----Thr----- 37
Db      1333 ACAGCAGTTTGGATGTTTGAACAACAGCCTTTGGACACAAATAAACAAAGACATCACAGAA 1392
Qy      37 ----- 37
Db      1393 ATTAAGTTGTTGAGGAATATCCATGGAGAAAATGTCAAAGTGGGTGGGTAGTAGACA 1452
Qy      38 -----Phe-----Pro----- 39
Db      1453 AAGTGGTTATTGAACTCAACCACTCGAGAAATCAAGAGAGTCAAGCGAGGCTGTC 1512
Qy      40 -----LysAlaMetAsp-----Asn 44
Db      1513 CTGAAAAACAGACAGTCATAGGTACAGATGTTTCTTAAAGAGTG-TTGGATGTTTGAAC 1571
Qy      45 -----ValThr-----ValThr----- 46
Db      1572 ACAGCCATTAGACATTTCTAAAGACTCTCTGTATACGACAGTGTATCATCTGAGAGAG 1631
Qy      47 -----Val----- 47
Db      1632 AATAGAGGTGATGTAAAGACCACCAACATCTATTGAAACACTCCCAATAGAGGCTTT 1691
Qy      48 ---ArgGln----- 49
Db      1692 AAAGACAGCCCGGATATCGAAAGCTTCAAAAATTCATCTGCTCTGAGAGAAAAGGG 1751
Qy      50 -----Gly----- 50
Db      1752 GGATGTTAAGCACCAAAATGGGTTTTTGAACCTCAACGCTTAGAAGATATTAGAGAGA 1811
Qy      51 ---Glu-----Ser-----Ala-----Thr----- 54
Db      1812 TAAGAAAGATACACCAAGAACAGTGGAGCTTAGAAGCAGTTGATAGAGGACATGTAAAGAA 1871
Qy      55 -----LeuArg----- 56
Db      1872 CTACACTCATATCTCGAATCCCAATATCTAATTAAGTTGACGCATCATCAAAATTGA 1931

```

QY 57 -----Cys----- 57
Db 1932 GGTAGAGGAGTCACAGAGCCACTGTGGAGTTGAATAAATCTCTCTTTGAGACAACCCC 1991
QY 58 Thr----- 58
Db 1992 ACTCTATGCCATTCAAGATCATCTTGGAAATAACCCAAAGTAAAGACAGTCCAGCAAGA 2051
QY 58 ----- 58
Db 2052 AGAATAGTAAGAGGTGATGTAAGAGCTGTAGATGGCTTTTGAACAAGGCTATTGA 2111
QY 59 -----Ile---AspAsn----- 61
Db 2112 CCAATTTGATGAAAGCCTTCATAAATTTCAAGATTTAGAGGAATATCTGCTCAAGHAAT 2171
QY 62 -----Arg-----Val----- 63
Db 2172 ACAGGCGGAATGTGAATCTGCTAGGTGTTTATTGAGACCCCAACCCCTTGATTCAT 2231
QY 64 -----Thr----- 64
Db 2232 TAAATATTTAGTAATGTGAAGAAACAGACAGCAAAACTGAACAAAGTACTGATATTGT 2291
QY 64 ----- 64
Db 2292 TAAAGGGGATGTCAAAACATGTAAATGGCTATTGAGACCCAGCCCAATGGAGTCTCTTTA 2351
QY 65 -----Arg----- 65
Db 2352 TGAAGAGTTCCTTGATGACCAACTCTGAAGATATTATAAGGTGATGTTAGAACCTG 2411
QY 66 ---Valala----- 67
Db 2412 CATGTGGCTGTTGAAACTCAGCCACTGTATGCCATTAAGATGACTCTGAAGCAACAGT 2471
QY 68 -----Trp----- 68
Db 2472 AAACTGCAAACTGTGAAACAGGAGGAGATACAAAGTGGGGATGTTTCAGACACATGTTT 2531
QY 69 ---Leu---AsnArg---Ser----- 72
Db 2532 TCTTTTGGACAGCAAAATCTGCACACATACAGGGGGATGAAGGGAAAGAAATAAGCC 2591
QY 73 -----Thrile----- 74
Db 2592 CTTGGAGATGATATACAACTCTGGGATGCTCTGCGCATGAAGTTTAAGTTTGAATAATCA 2651
QY 75 -----LeuTyr----- 76
Db 2652 GTCCTTAGACTCTATAAATTGCAAGTTTCAAGATGTTCTAAGTAAGATCAAAACGCTAAA 2711
QY 77 -----Ala----- 77
Db 2712 AGCCGAAGACATTCAGAAAGGCAATGTTCTAAATGCAGGTGCTATTGTAACCAACACC 2771
QY 78 -----Gly---Asn----- 80
Db 2772 TATTGATATGATAAAGAAAGTCAAGAAATGATGATGATGTTGGTTAAACACAGTGACAGCT 2831
QY 81 ---LysTrp---Cys-----Leu-----Asp 85
Db 2832 ACAAGGTGGAGATGTAAGAAAGGATGCTTCAATTTTGACACATTTCTTTAGATGAGAT 2891
QY 85 ----- 85
Db 2892 TAAAGATGATCCGATGGCATCGCATGAGAGAAACAAATCTCGGGGAATATAAAGG 2951
QY 86 -----Pro 86
Db 2952 TGATGTGAAAGCTACAAAATGCTTTTGAACACAAACCACTCTATGCAATTCAGACCA 3011
QY 87 ---ArgVal----- 88

Db 3012 TGAAGGGTTTTATCATGAAGTGAACAACAGTTTAAAAAAGAGAAACAATACATCGAGATGT 3071
QY 89 -----Val---Leu-----LeuSerAsnThr----- 94
Db 3072 ACCAGGAAACAAGGTGGCTCTTTTGAACAAAACCATTAGACTC---AATTCACCAATCAGA 3128
QY 94 ----- 94
Db 3129 AGATGTATACGTTTAAATCCGTCACCAGGAAGACATTCAGAGGGGGATGTGAGTTC 3188
QY 95 -----Gln-----Thr-----Gln----- 97
Db 3189 TGTCAATACAGGTTTGAAGAACTCAACCACTGGATATGATTTTCAGACAAATCCCATATAT 3248
QY 98 -----TyrSer-----Ile--- 100
Db 3249 TGTGCCCACTGTTGACTATATTCAAGGAGGCAATGTGCAGATGAATAACAATATTATGA 3308
QY 101 -----Glutlle----- 102
Db 3309 GTCTGAAGGTGTAACAAGAAAGAACTATGTAAAGACAGTAAGTGTCAATGAATAACAAA 3368
QY 103 -----GlnAsn----- 104
Db 3369 GGGCAATGTAAGACTTCTACTTGGCTCTTTGAAACTCAGAAATAGATGAGTTGGGAGA 3428
QY 105 ---Val-----Asp----- 106
Db 3429 AGAGTCCAGATATGAAAATATCAAGACAGTCAACCAGGAAGAGCTGCAGAAAGGTGATGT 3488
QY 107 -----val----- 107
Db 3489 GAAGCAAGCAGTGTGGCTTTTGAACACAGACTTTTGGATTCTATTAAATGAATCTGATGA 3548
QY 108 ---Tyr---Asp----- 109
Db 3549 AATGATACCAAAATGACAAAGAGAAATTCCTCGTCGGATGTCAAGCAACTACTAGTG 3608
QY 110 -----GluGly----- 111
Db 3609 GCTCTTTGAACAAACACCTATTTCAGCAATTTAAACAAACTAGAGTAGAAGAGGAAGAAAT 3668
QY 112 -----Pro----- 112
Db 3669 TATTGGTAAAGTATTAAAGAAACCTTGAAGACCTTCTACTCTCAAGAGATTGTTGAAGC 3728
QY 113 ---Tyr---Thr---Cys-----SerValGlnThr 119
Db 3729 TCCCGGAATTAATCATTTGAAGCTGATGAAGTTGGAGATGTGCAAGTGGCCAAATACAGCT 3788
QY 120 -----AspAsn----- 121
Db 3789 CATGAACCAACAACTCTCTGAGATCCAGAAAGGAAGATTTATCAGGGCTGATCTCGGAA 3848
QY 122 ---His-----ProLysThrSerArgValHis----- 129
Db 3849 CATCATGATGAACCTGCTTTTCCCAAG-----AGACTGCACAAAGAAAGAGATATTGT 3902
QY 130 -----Leu-----IleVal---GlnVal--- 134
Db 3903 CAGTGAAGGAGAGAGGAAACGTCATTTTACTAAACTCAATTTATTAACAGATCGAT 3962
QY 135 -----Ser---ProLys 137
Db 3963 GGAATTTTCATGCTGAAAGAGAGATAGTGAGAGGGGATGTAAACCAAGCAATCCAAA 4022
QY 138 IleVal-----Glu-----Ile----- 141
Db 4023 GCTGTCTCAGAGGAAGCGGTGCAAGAAAGGCATATTAAATTCAGAAAGATGAAGAGG 4082
QY 142 -----SerSer-----Asp----- 144

QY 220 ---Asn---TyrPro----- 222
Db 6297 GGAATTAAGGCTACCTCTCAAAGGATCAGAAAAGATCAATGTGTGCAATGACAGCTGA 6356
QY 222 222 222
Db 6357 GCACAGAGACAAAGCAAGATGTGTCGAAAAGGTCTTGTGTGAAGAAAACAGCTGCC 6416
QY 222 222 222
Db 6417 TGTTGACTCTCAAACTCGCTCTCTCAGACAGTTCCAGAAATCCAGACACCACCAAGAAA 6476
QY 223 ---ProTyrIle-----Ser 226
Db 6477 ACAGACAGCACCCCTGTGTAATCCCACTCATTCCTCCATCAGGTTTCAAGAACCAAAAGTCC 6536
QY 227 ---Glu----- 227
Db 6537 TAAGCCTTACATGAGGAAATTTAAGACACCTTTAATGATTCGTGAAGAAAATACAGACA 6596
QY 228 AlaLysGly-----ThrGly----- 232
Db 6597 GCAAGGGAAGAGCTTGAGAAACAGACAGAGAGTTCTTCCACAAATGTCTCAAAAC 6656
QY 233 ---ValPro-----Val----- 235
Db 6657 AGAAACAGACCAACAAAGCTTATCAGAGAGGAGGAAGAAATAGAGTTTACAAAAGCGAC 6716
QY 236 ---Gly-----GlnLys-----GlyThr----- 240
Db 6717 TGAGGCAATCTCCACACCCAGAAAGGAGTCAGACTTCTTAGGGCACGGCCCAACCTGGA 6776
QY 241 Leu-----Gln-----Cys----- 243
Db 6777 CTCTGAAGCAGGCTGTGATTGTCAGGTGAATGCTCTGAAGCCAACTCGCCACAGCTTC 6836
QY 244 ---GluAla-----Ser-----Ala 247
Db 6837 TACATTGACAGTAGCTACTAGAGGCTCCAGCATGTTCTAGCCGCTTCTGAAGATGAGCT 6896
QY 248 ---Val----- 248
Db 6897 TACCTTGAGACAGGAAGGCATCCAGACTCAAGTGATGCTTCAATCAAAATTTGGTTG 6956
QY 249 ---Pro---Ser-----Ala----- 251
Db 6957 TGAACCTAGCCAGAGTCACAAAGAAATGCAAGGCACAGCAAAATTTTGAGCAGCATGTGAA 7016
QY 252 Glu-----PheGln-----Trp----- 255
Db 7017 GAGACTGCCCTTTCCCAAAACCAACCCAGTTCGCCCAAGTTTCAAAGTGAAGAACTATCAA 7076
QY 255 255 255
Db 7077 GCITTCAACTCTAGATCACACAGGACTGAAAAGATCTTAGTCTTAAGCACCACCAAA 7136
QY 256 ---Tyr----- 256
Db 7137 GCAATCTGAAGTTGACATTCAAACCAAGTACTGAACAAACAGATAAGGAATCAAGAAAAC 7196
QY 257 ---Lys----- 257
Db 7197 CCAGGCNAGCATACAGTGTGATGATAGCCATCTGTGCTCGTGAAGAAATATTTTCAGTTACC 7256
QY 258 ---Asp----- 258
Db 7257 TAAACACAGAAAACGGGTGACCATACAAATGCCCAAGAAATATGCAGAGAAAGTCAATA 7316
QY 259 ---Asp-----Lys---ArgLeuIle----- 263
Db 7317 AAGTAAGTCCAGACAGATTCCCAAGGAAGCAAGGAATATTTGGGGAGTTTGACAGAGGAA 7376
QY 264 ---GluGly----- 265

Db 7377 TGTCTGGGAGGAGAGAAAATCAGGACTCTCTCGTGAGCTGTTCAAAGAAGACAG 7436
QY 266 ---LysLys-----Gly-----Val----- 269
Db 7437 ACTAATAGATGAAGAAAGCAAGAACATCTGCAGAACCCAGAGGGTACCAAGGTCAGTCCA 7496
QY 269 269 269
Db 7497 ACAAAGGTTATCAATGAACGCTTGGACTCACAGATGCAGAAATTTTCAGCAGACAGAAAT 7556
QY 270 ---Lys-----Val----- 271
Db 7557 ACRAACTTCTAGAGTACAAATTTGAGTGTGAAGAATTTCTCCAGTCTTACAATGCTACGCA 7616
QY 272 ---GluAsn----- 273
Db 7617 AGAGAAAACATGCTTAAAGACAAGGGCAACACAGGACAGGTCACTCTACACTGA 7676
QY 274 ---Arg-----Pro-----PheLeu----- 277
Db 7677 AGAGTCAAAGCAAGAGCTAAGACAGAACCAATCTGCATTTTCTCTGTGAAGATTCOCCA 7736
QY 278 Ser-----LysLeuIle----- 281
Db 7737 GCACGATGATGAAGAAATGTACCATAATATATTTGGAATTTCTTGGAAAACGTCGAGAACT 7796
QY 282 ---Phe----- 282
Db 7797 ACAGCAGATTTTCTTAGGGTAAACAGATTTGAAGCAGAGTCAAGTAAAGTGCCCTTAA 7856
QY 282 282 282
Db 7857 AACGTTTCAGATACTGTTAAATATTTGTCGCTATGCTGATAAGTGAGGAGAAAAGAGA 7916
QY 283 ---Phe----- 283
Db 7917 ATATGGAGTTTCGTTGCCATGAGGAATATTTTCGAAAAGTCAAGAGAGAAATACACA 7976
QY 284 ---Asn-----Val-----SerGlu---His 288
Db 7977 TATTAAGACTCAAGCCGAGAGATGCTTCTTCAGTGTGAACATGTAAATTCAGACAGCCAT 8036
QY 289 Asp-----Tyr----- 290
Db 8037 GATGGCTTCCCAACAGGAAGCAGAGAGATAAACCTTACCACTTAATGAATGTCACCT 8096
QY 290 290 290
Db 8097 GAATGTGCTTAATGTTAATCTCAGTCTGAGTAAATGCACGACAGAGAAAAGTAAAC 8156
QY 290 290 290
Db 8157 TGTAAGAAAATTAACACACCGACAATTAACACTCATCTCTGAGGAGCAACCCGTAA 8216
QY 291 ---Gly----- 291
Db 8217 TCTGTGTTAAACCATACCAGAGGCTTAAGGGGAGAGCGTAAGATGGCTCTCTCCCTCTTT 8276
QY 291 291 291
Db 8277 GAAACTCGCCCTCCATCACCAACTTTCATTACATAGAGTCCACTGCGCGTAGACAGA 8336
QY 292 Asn-----Tyr----- 293
Db 8337 AACCTCCAGAGAGTGAAGCTTTTCAGTCCCTTAAATAAACCGTTGTATTGAACCTCC 8396
QY 294 ---ThrCysVal----- 296
Db 8397 ACCCGAGACCGGTGGAACATGATCTGGACTTCCAGATCAAGAACACCCACTTCCCC 8456
QY 297 ---Ala----- 297

```
Db 8457 ACCAAGGAGTCGTTTCAGAACAACTTGTTCAGACTCAAGACACACCGCCAGGCTACGCCAA 8516
Qy 298 -----SerAsn-----LysLeu---Gly 302
Db 8517 AGGCACCATCCCTGTTGTTACACAGAACCCAGTTCATATTGTAGAGAAGAGATCTGAGGT 8576
Qy 303 -----His-----ThrAsnAla-----Ser----- 307
Db 8577 TGTTCATGTCCTCCAGCCACACTCCGCAGACAAATCAGATAGAAAGTGTGGTGGGACTC 8636
Qy 307 ----- 307
Db 8637 ACCACCCACCATCACAAATACCTGTGAGTCTAAACACAGTCGTGTAGTGGCTCTTCAGAGA 8696
Qy 308 Ile-----Met-----Leu----- 310
Db 8697 ATCTGTAGAGCTCAAGAGCGAGTGMAGAAAACAGAAAACGGAGACTTATGTTTCATAA 8756
Qy 311 -----Phe----- 311
Db 8757 AGACAAATGAATTCGTCAACAGAGCAATGCCAGAGACTGAAGCTACGATCGACGTGA 8816
Qy 312 Gly---Pro---Gly---Ala---Val---Ser---GluVal----- 319
Db 8817 AATCATCCGAAAGGTGGAGGGCCGCCACTATCAGAACACACAGAGAGATTGGAAGCCAC 8876
Qy 320 ---SerAsn---Gly---Thr----- 323
Db 8877 CAATCAACTGTTCAAGGGCTGAACGTTTCTGTAATGCCATGAAGAAATGAATAAAG 8936
Qy 324 ----- 324
Db 8937 ATGGTTTAGGGAATTTGAGATGACCCAGTTCAGAGCAAAAACAGAGAGAGACTTA 8996
Qy 325 -----Arg----- 325
Db 8997 TGCAAATGGCGAAATAAACCACACATGAAGAACAGAGAGTCAACATTTTGCAGAGAGGA 9056
Qy 326 -----Arg----- 326
Db 9057 ATTTGGATTAGCATCTTCGAACCTGCTAAATTTACAGCTTTTCTTACAGACATCGAA 9116
Qy 327 -----Ala----- 327
Db 9117 AGTTCCTGAATGCAGCCAGGGTTCACTCTGAAGCAAGTCTCTGAATGAGCAATTTCTC 9176
Qy 328 ---GlyCys---Val----- 330
Db 9177 GAGCGTGGATGCATTTGACAGTCAGATGTTGGGTCAAAGGTAGCAACCTCATCATCTCG 9236
Qy 331 -----Trp-----Leu---Leu-----ProLeuLeuVal---Leu 338
Db 9237 GAGCACAGAAGCTGGCAGATCGGCTTTGACTTCAAGCATGCCC-----ACCAGCCTA 9290
Qy 339 -----HisLeu-----Leu---Leu----- 343
Db 9291 TGAAGATGCATCTCTGCGCCACATCCTAGATGTGTCAGATTTCACCTACAAACCTCAGACG 9350
Qy 344 ---Phe 344
Db 9351 GAAATT 9356

RESULT 30
AY404089
LOCUS
DEFINITION
Pan troglodytes SACS gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY404089.1
VERSION
AY404089.1
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
REFERENCE
AUTHORS
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
1 (bases 1 to 11490)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
AUTHORS
2 (bases 1 to 11490)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..11490
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>11490
/gene="SACS"
/locus_tag="HCM1774"
gene
Alignment Scores:
Pred. No.: 2.92e-12 Length: 11490
Score: 1662.70 Matches: 278
Percent Similarity: 11.64% Conservative: 44
Best Local Similarity: 10.05% Mismatches: 11
Query Match: 69.05% Indels: 2434
Gaps: 239
US-10-017-084A-523 (1-344) x AY404089 (1-11490)
Qy 1 MetLysThrIle-----Gln-----Pro----- 6
Db 39 ATGCTATCCATTTGATGAAACAGAAATCACCCATCTGTTTCATGGCTTAAGATGTTG 98
Qy 7 ---Lys----- 7
Db 99 GAAAAATCTTTATATACATTTTTCAGAGGATTTGACTTTATTTGATGAGATGCCACTTAT 158
Qy 8 -----Met-----His-----AsnSer 11
Db 159 CCCCAGAACTACTAGAGGAGTCAACATGTGTGGAACTCATTAGACTCAGGATTC 218
Qy 12 Ile-----Ser----- 13
Db 219 ATCGTTAGTCATTTTAGACGATGAATCTGAAGACACAGCTTCCAGAAATTTTAGCAGACAT 278
Qy 14 -----Trp-----Ala 15
Db 279 TGTACAAAACCTTGGAGGGTTTGTCTTAAATAAATTAGATGCATCTATATACATCCGCT 338
Qy 16 -----Ile-----PheThr-----Gly----- 19
Db 339 TATTAAAAATATATTTCATTCACCATTCACCAAGTGTGTTTGCAGNATATGAGAGAT 398
Qy 20 ---LeuAla-----AlaLeu-----Cys--- 24
Db 399 GCCATTGCGAAATTTGTGAATGAATAACTTCGCTACTTCCCAACACACAAAGATGCCCT 458
Qy 25 -----Leu-----Phe-----Gln----- 27
Db 459 GAGAGAGTTCTTGCTAGTTTAAACCGATAGCAGTGAAGAGAGNNNNNTTATTCAAGN 518
Qy 28 ---Gly----- 28
```



```

Db 519 NTGGCAATATTNNNGCATNNNNNTCTCTGATCANNNATTCTCTTATACANN 578
Qy 28 -----
Db 579 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 638
Qy 28 -----
Db 639 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 698
Qy 28 -----
Db 699 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 758
Qy 28 -----
Db 759 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 818
Qy 29 -----Val---Pro---Val 31
Db 819 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 878
Qy 32 ArgSerGly---Asp-----AlaThr--- 37
Db 879 ---ACAGAAACAGATGATATCAGCTGTGAACTCTTTGACCCGTGATAGAACTACTAAA 935
Qy 38 -----PhePro----- 39
Db 936 GGATCTCTTTGTAAAGAGAGAACCTATTTCACCCTCAGTTTTCCTCACCAGA 995
Qy 40 -----LysAlaMetAsp-----AsnValThrValArg----- 48
Db 996 TATTCTTCACTCTTAAAGACA---GATTGGTTTAAAAA-----CGAAGCCAGTCT 1043
Qy 49 Gln-----GlyGlu-----SerAlaThr-----Leu 55
Db 1044 CAAAGAAAAGAGATGTTGTGGAAGTGGCAAAAAAATTAAGACCTTACAGGTCGGTCTG 1103
Qy 56 -----ArgCys-----Thr----- 58
Db 1104 TCCTGATCAAGATGTTCTTCTGAAGAAAGCAAAACCTCTTACTGGTTTAAATAAGAA 1163
Qy 59 -----Ile-----Asp-----Asn----- 61
Db 1164 TCACACACTGTTGCAATCATCTGAAGAAAGATGACATTGAAGAAATAAATAGGGTTC 1223
Qy 62 -----Arg----- 62
Db 1224 AGCTGCAAGAAAGGCTCCAATATATCCAGGCTCTTGGTCTGGAAAGGAGATCTCTG 1283
Qy 63 -----ValThrArg---Val-----Ala---TrpLeu--- 69
Db 1284 TAATCTCTGCAACCAACAGATATGTTGATGTAGGCCATGCANNICTCATTTGGCTCC 1343
Qy 69 ----- 69
Db 1344 ACTTCCTCTTGTGAAAGTATCCATGATTAACCTGGAAAGAACATTAGGATCTTCACAAA 1403
Qy 70 -----Asn----- 70
Db 1404 ACCTAGCCTTAGTCTGTCTTAAAAACACTNTAAATTTGTTGATGGTATTCTTCAAA 1463
Qy 71 -----Arg-----Ser-----Thr-IleLeu-----TyrAlaG1 78
Db 1464 NACCTTTAGTGATGAAGACTACTATCAATTCAGCATATTTTCTGTTGAATTTAC---GG 1520
Qy 78 y-----Asn-----Asp-----Lys----- 81
Db 1521 ATTCATGCATGATCATCTTAATAAGAGGAAGATCTTTTAGANNNTAAATTTCCATG 1580
Qy 82 ---Trp-----CysLeuAspPro-----Arg---ValVal----- 89

```

```

Db 1581 GGTTGGACTGGCAAAAGTTTGT-----CCACTTGCCAGGCTGTGATTAACCAAT 1634
Qy 90 -----LeuLeuSerAsn-----Thr----- 94
Db 1635 CCATGATNNNNNNNCTTCAGNNTTATTGCAATATGNNCTTAAACACCATGGCAAAATTC 1694
Qy 95 -Gln-----Thr----- 96
Db 1695 CCAACTATTAAAGTCTGTGGTTCATAGAGGAGTTGCATCATCATATTTCCATGGT 1754
Qy 97 ---Gln-----Tyr-----Ser-----Ile-----Glu----- 101
Db 1755 TATTGAGAAGATATCTCAAAAGTGACCAAGATCTCAGTGAACAGAAAGCAACAAAA 1814
Qy 102 -----Ile-----Gln----- 103
Db 1815 TCTTCATCTTATGTTGAATATTATCAGATGGCTATATAGCAATCAGATTCCAGCAAGCCC 1874
Qy 104 -----Asn----- 104
Db 1875 CAACACACAGTTCCTTATATCATATAGCAAAAAATCCTTTAAACTTATCATGAAGCCAAT 1934
Qy 105 -----ValAsp----- 106
Db 1935 TCAGGAATGCTGTTATTGTGACATTAAAGTTGATGACCTTAATGACTTACTTGAAGATTC 1994
Qy 107 -----ValTyr-----Asp----- 109
Db 1995 TGTGSAACCAATCATTTTGGTGCATGAGGACATACCCTGAAAACTGCAGAAATGGCTAAA 2054
Qy 110 -----Glu----- 111
Db 2055 AGTTCCATGCCTTAGTACAAGACTGATATAATCTCGAAAAACATGGGATTTGAGCAGTCAG 2114
Qy 111 y-----Pro-----Tyr----- 113
Db 2115 ACAAGAGAGGCCACTTACTGTAGAATTAATAATATTCTGGAAGATATACCTTCAGTGTG 2174
Qy 114 -----Thr-----CysSer--- 116
Db 2175 AGATATTTTAAAGAACTACTTCAAAACGCTGATGATGCAAAATGCAACAGATGCAAGTTT 2234
Qy 117 -----Val----- 117
Db 2235 CTTGATTTGATATGAGAAGAAATATGCACATAGAGAGAAATCTCTAGACCCAGGATGGC 2294
Qy 118 -----Gln----- 118
Db 2295 AGCTTGTCTAGGACCTGCTTTTGTGTCATTCAACAATTTCTCAATTTCTCAGATTCAGATT 2354
Qy 119 -----Thr-----Asp----- 120
Db 2355 TGTGAACATACTAGGTTAGGAGAAATCTTTAAAAAGGGGAGAGTTGACAAAAGTTGGAAA 2414
Qy 121 -----Asn-----His-----Pro-----LysThrSe 126
Db 2415 ATTTGCTCTGGATTAAITCTGTGTACCATATCTACTGACATTCCTCATTTATG---AG 2471
Qy 126 rArg-----Val-----His----- 129
Db 2472 TCGGAATTCATGATAAATGTTGATCCAAACATAAATCATATCAGTAAACACATTAAAGA 2531
Qy 130 -----Leu----- 130
Db 2532 CAAATCCAAATCCTGGGATCAAAATTAATTTGGAGTAAACAAACAGAAAGACTTTAGAAAAT 2591
Qy 131 -----Ile---Val-----Gln-----Val--- 134
Db 2592 TCCTAATCAGTTCAACCAATTTATAGATGTTTGGCTGTCTGACTTACCTTTGACTGTAGA 2651
Qy 135 -SerPro----- 136
Db 2652 AGCAGCTTACAGCTATAAATGGAACTCTTTTCGACTGTCTTTTAGAACTCAACAGGAAGC 2711

```


5949	Db	TGGGGCAGAACTTCTCATGTTTCTTAATCAGTCGAAAAAAATTTCTATTGTGGAATAGA	6008
252	Qy	-----	252
6009	Db	TAAGAGTACTGGAGCTCTAAATGTGCTGATTTCAGTAAAGGGCAAAATTCACAGATGGAGA	6068
253	Qy	-----Phe-----	253
6069	Db	CAGATTGAAAGGAAACAATTTCTATGTCATCTGTAATTGATAGTGTGTACTAAAAAGAGCCA	6128
254	Qy	-----Gln-----	254
6129	Db	GCTCAAGACATACCAGTTCAACAAATAA CCTATACTATGGATCTCAGGACTCTGAAGG	6188
255	Qy	-----Trp-----	255
6189	Db	AAATCTTACTACGTGGCTAAATTTGTAATAGATCAGGCTTTTCAAGTATGGAGAAAGTATC	6248
255	Qy	-----	255
6249	Db	TAAGAGTGTCAATCAGCTCAACAAGAACCAAGATATTACTCTTTTCCCAGTGGTGGAGT	6308
256	Qy	-----TyrLys-----	257
6309	Db	AGTGCCTGCATTACTCACAACATATAAAAAACCCCATAGGGCCTTCGTGTTTTTGGCTCT	6368
257	Qy	-----	257
6369	Db	TTCTTTGGAGACTGGGTGCCATTTTCATGTGAATGGCCACTTTTGCATCGATTTCAGCCAG	6428
258	Qy	-----AspAspLys-----Arg-----	261
6429	Db	AAGAACTGTGGCGTGAATGATATGAGAGTGGTGTGCGAAGTGA CTGGAATTAACAGTTT	6488
262	Qy	-----LeuLeu-----Glu-----GlyLysLys-----	267
6489	Db	AATGACAGCATTAATAGCTCCTGCTATGTGTAATGCTAATACAGTTAAAAACGGTA	6548
268	Qy	-----Gly-----Vally 270	270
6549	Db	TTTCCCTGGTCTGATCCAACTATTCAGTGTTCAGAAACACCCCTATTTCATGTTGTAAA	6608
270	Qy	s-----ValGluAsnArg-----Pr 275	275
6609	Db	GGANNNTTAAAGAAGTTTTTATCGTTTTTCCAGTT--AACCGTCTGATCTACAGCC	6665
275	Qy	o-----Ph 276	276
6666	Db	AGATTATATTGCTACTGAAAGCACTTTACAATTTGCATTCAGAAAGACATGAACGTCT	6725
276	Qy	eLeu-----SerLysLeu-----280	280
6726	Db	TTTACCTGTGTGGGGCTCCAAATATTGATGCTCTGACTCTGCATCTGCACTGTATAAT	6785
281	Qy	-----Ile-----PhePhe--AsnVal-----285	285
6786	Db	TACTTGGATCAATATGTCATTTCAATAAATAAACTAGACCACTTTTGTGCAATTTACTACA	6845
286	Qy	SerGlu-----His-----AspTyr-----290	290
6846	Db	GGATGAATCAACACACCTTAAAAAATGCAGATTATAATATCACCACACGCAAAACACTAGC	6905
291	Qy	-----Gly--Asn-----Tyr--293	293
6906	Db	AGAGAATGCTATAGGCTGAACAATCTCCCTTTAGAAATTGGTTTCAACTTGGTTTATAA	6965
294	Qy	-----Thr-----Cys-----295	295
6966	Db	CTGTGATGAACCTGCTAACTTTTACCACCTGCTTATAGATGCAGATATTCCTGTGTAGTTA	7025
296	Qy	-Val-----Ala-----Ser-----298	298
7026	Db	TGTGACCCCTGCTGATATCAGATCTTTTTTAATGACATTTTTTCTCTCTCCTGACACTAAATG	7085

```
QY 299 -----Asn----- 299
Db 7086 CCAATTGGGAAGCTGCTGCTGCAGCAGACTAATCTAAACATTTTTCATAGTTT 7145
QY 300 -LysLeu-----G1 302
Db 7146 AAAAAGCTTTAGTTGATTGTTTAAAGATGCAGAGAAAATGAGATTGAAGNNGAGG 7205
QY 302 Y----- 302
Db 7206 ATTGCCCNFTCTCATCAANNNNACAGTGTGTTTGCAAACTTNNGATGCAAAACGACCAA 7265
QY 303 -----His-----Thr-- 304
Db 7266 GTTTCCTAACACATATCATGAATTGATTCATCCCGCAAGACNNGTTTATGAATACATT 7325
QY 305 -----Asn----- 305
Db 7326 APATTTGAAATAGTAATATTTTATGAACTGTAAAGTTGCAAAAGTGTGACATTTC 7385
QY 306 -----Ala-----SerIleMet----- 309
Db 7386 CAGCTTGTGATTGTTATCCTCTGTGTGCTCGAATATAGACCAAAAGTTGCAC 7445
QY 310 -----Leu----- 310
Db 7446 AAGTGGAAGACAAATTTTGCAAGTGAGTCTTGCTTAAAGATGCATGGCATTATTATAG 7505
QY 311 -----phe----- 311
Db 7506 TGAATCTGAAGTGTGAAGAAGATCAGGAAGAAACAAACAACTTTGACATTGTTGT 7565
QY 312 -----Gly-----ProGly-----AlaValSer----- 317
Db 7566 TGATACTCTAAAGACTGGGCATTCCTCCAGGAACAAAGTTTACTGTTTCAGCAACA 7625
QY 318 -----Glu-----Val-----Ser----- 320
Db 7626 GCTTGTGTTCTCTGAAGAGAGATGTTCTGCTCTCTCAGCCTTATGCACATTGCGATT 7685
QY 321 -----Asn-----Gly----- 322
Db 7686 TCCAAATGCCAGAGTGATAAAGTTTTCATGCTCTAATGAAGCTGCTGTATTTCAGCT 7745
QY 322 ----- 322
Db 7746 TGCTTTGAACAAATTTGTTCCAAAGACAGTGCATTTGTTCTCTGTTGTCTATGCACAC 7805
QY 323 -----ThrSe 324
Db 7806 AGCAAAATATAGAGAGCCCCCAAGCATCTTGAAGSCTCTACATTATATATGTCCTCAAACTTC 7865
QY 324 r-----Arg----- 325
Db 7866 AACATTAGACGAGAAAAAATTAGTAGAAAAATGATTTGAGGCACCTTTTGATGTATTCAA 7925
QY 325 ----- 325
Db 7926 CTGCAATTTGAATCATTGTGCTCCAGATGATATAAAATTTCTAAAGTCACCTTCGCTG 7985
QY 326 -----Arg-----Ala-----Gly-----Cys----- 329
Db 7986 CTATAAATCCATCAGTGGCCGCTGATGAGCATTTGAAAAATTTGGAACATGCTAGTACT 8045
QY 330 -----Val-----Trp----- 331
Db 8046 TACAAAAAGTATCCCTTCAGCTGAAGTGGAGAAATGGACAAATCATCATCATCTGCATT 8105
QY 332 -----LeuLeu-----Pro----- 334
Db 8106 TCTTGAAGAAAAAATACACTTAAAGAACTATATAGAGGTGATTGGTTGTGTACCTGTAGA 8165
```

```
QY 335 -----LeuLeu-----Val----- 337
Db 8166 TGATCTTGAGGTATATTGTGAACACCTCTTACCCAAAATTTGAAAATCTCTCTTATGATGC 8225
QY 338 -----Leu-----HisLeu-----LeuLeuLys----- 343
Db 8226 AAAATTAGAGCACTTGATCTACCTTAAAGATAGATTATCAAGTCTGAGGAAATTATCAGA 8285
QY 344 -----Phe 344
Db 8286 GATTAAGGAACACACTTTTTT 8304
```

Search completed: May 28, 2004, 14:03:57
Job time : 3334 secs